

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

DATE: 12/16/93 TIME: 13:07:45

1 2		SEQUENCE LISTING
2 3 4	(1) G	eneral Information:
5 6 7	(i)	APPLICANT: Artavanis-Tsakonas, S. et al.
8 9 10 11	(ii)	TITLE OF INVENTION: Therapeutic And Diagnostic Methods And Compositions Based On Notch Proteins And Nucleic Acids
12 13	(iii)	NUMBER OF SEQUENCES: 21
14 15 16 17 18 19 20 21	(iv)	CORRESPONDENCE ADDRESS:  (A) ADDRESSEE: Pennie & Edmonds  (B) STREET: 1155 Avenue of the Americas  (C) CITY: New York  (D) STATE: New York  (E) COUNTRY: U.S.A.  (F) ZIP: 10036
22 23 24 25 26 27	(v)	COMPUTER READABLE FORM:  (A) MEDIUM TYPE: Floppy disk  (B) COMPUTER: IBM PC compatible  (C) OPERATING SYSTEM: PC-DOS/MS-DOS  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28 29 30 31 32	(vi)	CURRENT APPLICATION DATA:  (A) APPLICATION NUMBER: 08/083,590  (B) FILING DATE: 25-JUN-1993  (C) CLASSIFICATION:
33 34 35 36 37	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Misrock, S. Leslie (B) REGISTRATION NUMBER: 18,872 (C) REFERENCE/DOCKET NUMBER: 7326-015
38 39 40 41 42 43	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 212 790-9090 (B) TELEFAX: 212 8698864/9741 (C) TELEX: 66141 PENNIE
44 45	(2) INFO	RMATION FOR SEQ ID NO:1:
46 47 48 49 50	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 2892 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: unknown

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

DATE: 12/16/93 TIME: 13:07:51

52 53		(ii	) MO:	LECU	LE T	YPE:	cDN	A									
54 55 56 57 58		(ix	()		E: AME/I OCAT:			26	<b>4</b> 0								
59 60 61		(xi	) SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID NO	0:1:						
62	GAA'	rtcg	GAG (	GAAT'	TATT(	CA A	AACA'	raaa)	C AC	ATA	AACA	ATT	rgag'	rag :	TTGC	CGCACA	60
63 64	CAC	ACAC	ACA (	CACA	GCCC	GT G	GATT	ATTA	C AC	TAAA	AGCG	ACA	CTCA	ATC (	CAAA	AAATCA	120
65 66 67 68	GCA	ACAA	AAA (	CATC	AATAA	AA C									ACA Thr	GCA Ala 10	171
69 70 71 72 73					ACA Thr 15												219
74 75 76 77					AAG Lys												267
78 79 80					AGC Ser												315
81 82 83 84 85					ACG Thr												363
86 87 88 89					ACC Thr												411
90 91 92 93					AAC Asn 95												459
94 95 96 97					ACG Thr												507
98 99 100					TCG Ser												555
101 102	AGC	GGC	AAT	GCG	CGA	ACC	AAC	AAG	CTC	CTC	ATC	CAG	CGA	CTC	TTG	GTG	603

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DATE: 12/16/93 TIME: 13:07:57

103 104 105	Ser	Gly 140	Asn	Ala	Arg	Thr	Asn 145	Lys	Leu	Leu	Ile	Gln 150	Arg	Leu	Leu	Val	
106 107 108 109															TCG Ser		651
110 111 112 113															GAT Asp 185		699
114 115 116 117															GAC Asp		747
118 119 120 121															TGT Cys		795
122 123 124 125															AAA Lys		843
126 127 128 129															CAA Gln		891
130 131 132															AAC Asn 265		939
133 134 135 136															GAG Glu		987
137 138 139 140 141															AAC Asn		1035
142 143 144 145															GGA Gly		1083
146 147 148 149															GAA Glu		1131
150 151 152 153															GGT Gly 345		1179

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154 155 156 157	TGC Cys								1227
158 159 160 161	AAC Asn								1275
162 163 164 165	GAC Asp 380								1323
166 167 168 169	GGA Gly								1371
170 171 172 173	GGA Gly								1419
174 175 176 177	ATA Ile				 	 	 	 	1467
178 179 180 181	GGA Gly								1515
182 183 184 185	CAC His 460								1563
186 187 188 189	CGC Arg								1611
190 191 192 193	GTT Val								1659
194 195 196 197	AAT Asn								1707
198 199 200 201	AAG Lys								1755
202 203 204	AAC Asn 540								1803

### RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

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DATE: 12/16/93 TIME: 13:08:11

205																	
206			AAT														1851
207	Cys	Ala	Asn	Gly	Phe	Arg	Gly	Lys	Gln	Cys	Asp	Glu	Glu	Ser	Tyr	Asp	
208	555					560					565					570	
209																	
210	TCG	GTG	ACC	TTC	GAT	GCC	CAC	CAA	TAT	GGA	GCG	ACC	ACA	CAA	GCG	AGA	1899
211	Ser	Val	Thr	Phe	Asp	Ala	His	Gln	Tyr	Gly	Ala	Thr	Thr	Gln	Ala	Arg	
212					575					580					585	_	
213																	
214	GCC	GAT	GGT	TTG	ACC	AAT	GCC	CAG	GTA	GTC	CTA	ATT	GCT	GTT	TTC	TCC	1947
215	Ala	Asp	Gly	Leu	Thr	Asn	Ala	Gln	Val	Val	Leu	Ile	Ala	Val	Phe	Ser	
216			_	590					595					600			
217																	
218	GTT	GCG	ATG	CCT	TTG	GTG	GCG	GTT	ATT	GCG	GCG	TGC	GTG	GTC	TTC	TGC	1995
219			Met														
220			605					610				4	615			- 2	
221																	
222	ATG	AAG	CGC	AAG	CGT	AAG	CGT	GCT	CAG	GAA	AAG	GAC	GAC	GCG	GAG	GCC	2043
223			Arg														
224		620	5		5		625				-7-	630					
225																	
226	AGG	AAG	CAG	AAC	GAA	CAG	AAT	GCG	GTG	GCC	ACA	ATG	CAT	CAC	AAT	GGC	2091
227			Gln														
228	635					640					645					650	
229											V - V						
230	AGT	GGG	GTG	GGT	GTA	GCT	TTG	GCT	TCA	GCC	TCT	CTG	GGC	GGC	AAA	ACT	2139
231			Val														2233
232		1		<b>1</b>	655					660			0-1	0-7	665		
233					000					000					003		
234	GGC	AGC	AAC	AGC	GGT	СТС	ACC	TTC	САТ	GGC	GGC	ממכ	CCG	Тαα	ΔТС	ΔΤΟ	2187
235			Asn														2107
236	1			670	<b>-</b> 1				675	<b>-</b> 1	<b>01</b>			680		110	
237				0.0					0,5								
238	ΔΔΔ	AAC	ACC	TGG	GAC	DAG	тсс	GTC	אאכ	ממכ	מידי∆	тст	GCC	тСΔ	GCZ	GCA	2235
239			Thr														2233
240	_10		685			_,_		690	11011			<b>-</b> 10	695	001	٠٠٠٠	1114	
241			005					0,50					0,5				
242	GCA	GCG	GCG	GCG	GCG	GCA	GCA	GCG	GCG	GAC	GAG	тст	СТС	ΔΤС	тас	CCC	2283
243			Ala														2203
244	1114	700	1114		1114	1114	705		1114	1100	<b>014</b>	710	104	1100	- y -	Cij	
245		, 00					, 03					, 10					
246	GGA	тдт	GTG	GCC	TCG	стс	aca	СЪТ	ממכ	ממכ	ידיממ	GCC	ממכ	тСΣ	GAC	ጥጥጥ	2331
247			Val														2331
248	715	- y -	var	AΙα	JCI	720	AIG	HSP	ASII	ASII	725	ALG	ASII	DCI	App	730	
249	, 1, 3					, 2, 0					, 23					, 50	
250	ጥርታጥ	CTC	GCT	ררפ	מידים	ממי	אמא	פככ	ΔAG	ጥሮር	CDD	AAG	CDD	רידירי	አአ <b>ሮ</b>	ACC	2379
250 251			Ala														4319
251	Cys	var	лта	FIO	735	GIII	лту	лта	пуъ	740	9111	пур	GIII	пеи	745	****	
252					, 55					/ <del>1</del> U					/43		
254	GAT	כככ	ACG	CTC	Δጥር	CAC	כפכ	CCT	ጥሮር	ככפ	GCA	GGC	∆מכ	тсъ	GCC	AAG	2427
255			Thr														444/
دري	rap	-10	* * * T	.u∈u	1.100	*****	7+9	Gry	JEL	-10	AIA	GTY	DGT	DEL	лια	пуэ	

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256	750 755 760	
257		
258	GGA GCG TCT GGC GGA GGA CCG GGA GCG GCG GAG GGC AAG AGG ATC TCT	2475
259	Gly Ala Ser Gly Gly Gly Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser	
260	765 770 775	
261		
262	GTT TTA GGC GAG GGT TCC TAC TGT AGC CAG CGT TGG CCC TCG TTG GCG	2523
263	Val Leu Gly Glu Gly Ser Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala	
264	780 785 790	
265		
266	GCG GCG GGA GTC GCA GCC TGT TCA TCC CAG CTA ATG GCT GCA GCT	2571
267	Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Gln Leu Met Ala Ala Ala	
268	795 800 805 810	
269		
270	TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG	2619
271	Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Arg Ser Val	2019
272		
272	815 820 825	
273	CEG EGG CGG ACE GGG CAE AEG ENAGEGGANN NAMEGGGANG GGGEGGEGG	0670
274 275	GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT	2670
	Val Cys Gly Thr Pro His Met	
276	830	
277		
278	AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGTT	2730
279		
280	GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTTGTTG ATTGAAGCAG TTTAGTCGTC	2790
281		
282	ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850
283		
284	TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2892
285		
286		
287	(2) INFORMATION FOR SEQ ID NO:2:	
288		
289	(i) SEQUENCE CHARACTERISTICS:	
290	(A) LENGTH: 833 amino acids	
291	(B) TYPE: amino acid	
292	(D) TOPOLOGY: unknown	
293		
294	(ii) MOLECULE TYPE: protein	
295	(all, stalled lands ground	
296	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
297	(, Dagodros Doodrat tion, Dag in No.2.	
298	Met His Trp Ile Lys Cys Leu Leu Thr Ala Phe Ile Cys Phe Thr Val	
299		
	1 5 10 15	
300	The Mel Cle Mel Mie Con Con Cle Con Phy Cle Tee Per Tee Tee	
301	Ile Val Gln Val His Ser Ser Gly Ser Phe Glu Leu Arg Leu Lys Tyr	
302	20 25 30	
303		
304	Phe Ser Asn Asp His Gly Arg Asp Asn Glu Gly Arg Cys Cys Ser Gly	
305	35 40 45	

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

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307 308 309	Glu	Ser 50	Asp	Gly	Ala	Thr	Gly 55	Lys	Cys	Leu	Gly	Ser 60	Cys	Lys	Thr	Arg
310 311 312	Phe 65	Arg	Val	Cys	Leu	Lys 70	His	Tyr	Gln	Ala	Thr 75	Ile	Asp	Thr	Thr	Ser 80
313 314 315	Gln	Cys	Thr	Tyr	Gly 85	Asp	Val	Ile	Thr	Pro 90	Ile	Leu	Gly	Glu	Asn 95	Ser
316 317 318	Val	Asn	Leu	Thr 100	Asp	Ala	Gln	Arg	Phe 105	Gln	Asn	Lys	Gly	Phe 110	Thr	Asn
319 320 321	Pro	Ile	Gln 115	Phe	Pro	Phe	Ser	Phe 120	Ser	Trp	Pro	Gly	Thr 125	Phe	Ser	Leu
322 323 324	Ile	Val 130	Glu	Ala	Trp	His	Asp 135	Thr	Asn	Asn	Ser	Gly 140	Asn	Ala	Arg	Thr
325 326 327	Asn 145	Lys	Leu	Leu	Ile	Gln 150	Arg	Leu	Leu	Val	Gln 155	Gln	Val	Leu	Glu	Val 160
328 329 330	Ser	Ser	Glu	Trp	Lys 165	Thr	Asn	Lys	Ser	Glu 170	Ser	Gln	Tyr	Thr	Ser 175	Leu
331 332 333	Glu	Tyr	Asp	Phe 180	Arg	Val	Thr	Cys	Asp 185	Leu	Asn	Tyr	Tyr	Gly 190	Ser	Gly
334 335 336	Cys	Ala	Lys 195	Phe	Cys	Arg	Pro	Arg 200	Asp	Asp	Ser	Phe	Gly 205	His	Ser	Thr
337 338 339	Cys	Ser 210	Glu	Thr	Gly	Glu	Ile 215	Ile	Cys	Leu	Thr	Gly 220	Trp	Gln	Gly	Asp
340 341 342	Tyr 225	Cys	His	Ile	Pro	Lys 230	Cys	Ala	Lys	Gly	Cys 235	Glu	His	Gly	His	Cys 240
343 344 345	Asp	Lys	Pro	Asn	Gln 245	Cys	Val	Cys	Gln	Leu 250	Gly	Trp	Lys	Gly	Ala 255	Leu
346 347 348	Cys	Asn	Glu	Cys 260		Leu	Glu		Asn 265		Ile	His	Gly	Thr 270	_	Asn
349 350 351	Lys	Pro	Trp 275	Thr	Cys	Ile	Cys	Asn 280	Glu	Gly	Trp	Gly	Gly 285	Leu	Tyr	Cys
352 353 354	Asn	Gln 290	Asp	Leu	Asn	Tyr	Cys 295	Thr	Asn	His	Arg	Pro 300	Cys	Lys	Asn	Gly
355 356 357	Gly 305	Thr	Cys	Phe	Asn	Thr 310	Gly	Glu	Gly	Leu	Tyr 315	Thr	Cys	Lys	Cys	Ala 320

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

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358 359 360	Pro	Gly	Tyr	Ser	Gly 325	Asp	Asp	Cys	Glu	Asn 330	Glu	Ile	Tyr	Ser	Cys 335	Asp
361 362 363	Ala	Asp	Val	Asn 340	Pro	Cys	Gln	Asn	Gly 345	Gly	Thr	Cys	Ile	Asp 350	Glu	Pro
364 365 366	His	Thr	Lys 355	Thr	Gly	Tyr	Lys	Cys 360	His	Cys	Ala	Asn	Gly 365	Trp	Ser	Gly
367 368 369	Lys	Met 370	Cys	Glu	Glu	Lys	Val 375	Leu	Thr	Cys	Ser	Asp 380	Lys	Pro	Cys	His
370 371 372	Gln 385	Gly	Ile	Cys	Arg	Asn 390	Val	Arg	Pro	Gly	Leu 395	Gly	Ser	Lys	Gly	Gln 400
373 374 375		_	Gln	_	405	_			_	410					415	_
376 377 378			Leu	420		-			425		-			430	_	
379 380 381	_		Pro 435			_		440	_				445			
382 383 384		450	Glu				455	-	-		-	460		-		
385 386 387	465		Thr	_		470					475		_		_	480
388 389 390			Phe		485					490					495	
391 392 393			Pro	500					505	_				510		_
394 395 396			Cys 515		_			520				_	525	_		
397 398 399	_	530	Asp		_		535	_		-		540	_	_		_
400 401 402	Met 545	Asn	Arg	Val	Asn	Ser 550	Phe	Glu	Cys	Val	Cys 555	Ala	Asn	Gly	Phe	Arg 560
403 404 405	_		Gln	_	565				_	570					575	
406 407 408	His	Gln	Tyr	Gly 580	Ala	Thr	Thr	Gln	Ala 585	Arg	Ala	Asp	Gly	Leu 590	Thr	Asn

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409 410 411	Ala	Gln	Val 595	Val	Leu	Ile	Ala	Val 600	Phe	Ser	Val	Ala	Met 605	Pro	Leu	Val
412 413 414	Ala	Val 610	Ile	Ala	Ala	Cys	Val 615	Val	Phe	Cys	Met	Lys 620	Arg	Lys	Arg	Lys
415 416 417	Arg 625	Ala	Gln	Glu	Lys	Asp 630	Asp	Ala	Glu	Ala	Arg 635	Lys	Gln	Asn	Glu	Gln 640
418 419 420	Asn	Ala	Val	Ala	Thr 645	Met	His	His	Asn	Gly 650	Ser	Gly	Val	Gly	Val 655	Ala
421 422 423		Ala		660					665		_			670	_	
424 425 426		Phe	675	_	_			680			_		685	_	-	-
427 428 429		Val 690				_	695					700				
430 431 432	705	Ala				710				_	715	_				720
433 434 435		Asp			725				_	730	-				735	
436 437 438 439		Ala	_	740		_			745		_			750		
440 441 442		_	755			-		760		-	_		765	-	-	Gly
443 444 445		Gly 770 Cys					775	_				780			_	
446 447 448	785	Cys				790					795		-			800
449 450 451		Gly			805					810				_	815	_
452 453 454	Met	<b>-</b> -7		820				3	825			<b>0</b> 12	<b>4-7</b>	830		
455 456 457	(2)	INFO	ORMA:	TION	FOR	SEO	ID N	IO:3:								
458 459			SEÇ													

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

DATE: 12/16/93 TIME: 13:08:42

460 461 462 463 464	<ul><li>(A) LENGTH: 1320 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: unknown</li></ul>	
465 466	(ii) MOLECULE TYPE: cDNA	
467 468 469 470 471	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 4421320	
472 473 474	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
475 476	CCGAGTCGAG CGCCGTGCTT CGAGCGGTGA TGAGCCCCTT TTCTGTCAAC GCTAAAGATC	60
477 478	TACAAAACAT CAGCGCCTAT CAAGTGGAAG TGTCAAGTGT GAACAAAACA AAAACGAGAG	120
479 480	AAGCACATAC TAAGGTCCAT ATAAATAATA AATAATAATT GTGTGTGATA ACAACATTAT	180
481 482	CCAAACAAAA CCAAACAAAA CGAAGGCAAA GTGGAGAAAA TGATACAGCA TCCAGAGTAC	240
483 484	GGCCGTTATT CAGCTATCCA GAGCAAGTGT AGTGTGGCAA AATAGAAACA AACAAAGGCA	300
485		
486 487	CCAAAATCTG CATACATGGG CTAATTAAGG CTGCCCAGCG AATTTACATT TGTGTGGTGC	360
488 489	CAATCCAGAG TGAATCCGAA ACAAACTCCA TCTAGATCGC CAACCAGCAT CACGCTCGCA	420
490 491 492 493	AACGCCCCCA GAATGTACAA A ATG TTT AGG AAA CAT TTT CGG CGA AAA CCA Met Phe Arg Lys His Phe Arg Arg Lys Pro 1 5 10	471
494 495 496 497	GCT ACG TCG TCG TTG GAG TCA ACA ATA GAA TCA GCA GAC AGC CTG Ala Thr Ser Ser Leu Glu Ser Thr Ile Glu Ser Ala Asp Ser Leu 15 20 25	519
498 499 500 501	GGA ATG TCC AAG AAG ACG GCG ACA AAA AGG CAG CGT CCG AGG CAT CGG Gly Met Ser Lys Lys Thr Ala Thr Lys Arg Gln Arg Pro Arg His Arg 30 35 40	567
502 503 504 505	GTA CCC AAA ATC GCG ACC CTG CCA TCG ACG ATC CGC GAT TGT CGA TCA Val Pro Lys Ile Ala Thr Leu Pro Ser Thr Ile Arg Asp Cys Arg Ser 45 50 55	615
506 507 508	TTA AAG TCT GCC TGC AAC TTA ATT GCT TTA ATT TTA ATA CTG TTA GTC Leu Lys Ser Ala Cys Asn Leu Ile Ala Leu Ile Leu Ile Leu Leu Val 60 65 70	663
509 510	CAT AAG ATA TCC GCA GCT GGT AAC TTC GAG CTG GAA ATA TTA GAA ATC	711

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511 512 513	His 75	Lys	Ile	Ser	Ala	Ala 80	Gly	Asn	Phe	Glu	Leu 85	Glu	Ile	Leu	Glu	Ile 90	
514 515 516 517				AAC Asn												CCA Pro	759
518 519 520 521				AGG Arg 110													807
522 523 524 525				CTG Leu													855
526 527 528 529		_		ACG Thr													903
530 531 532 533				AGC Ser													951
534 535 536 537				ACG Thr													999
538 539 540 541				ATG Met 190													1047
542 543 544 545				TCA Ser													1095
546 547 548 549				CAC His													1143
550 551 552 553				GCC Ala													1191
554 555 556 557				GAC Asp													1239
558 559 560 561				TGC Cys 270													1287

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562 563 564 565					GGC Gly												1320
566 567	(2)	INF	ORMA'	TION	FOR	SEQ	ID I	NO:4	:								
568 569			(i) :	e eati	ENCE	רשאו	ס א כייייי	יסדפי	TTCC								
570			(1)		) LEI						3						
571					) TYI												
572 573				(D	) TO	POLO	3Y: 1	unkno	own								
574		(:	ii) l	MOLE	CULE	TYP	E: p:	rote	in								
575 576		(-	xi) :	SEOU	ENCE	DESC	ים ד קי∼	יד	. SE	מד כ	NO ·	1 •					
577		\-	Λ <b>Ι</b> , Ι	3HQ0.	BINCE	DES	CICLE.	LION	. 014	עו ע	110.	<b>.</b>					
578		Phe	Arg	Lys	His	Phe	Arg	Arg	Lys		Ala	Thr	Ser	Ser		Leu	
579 580	1				5					10					15		
581	Glu	Ser	Thr	Ile	Glu	Ser	Ala	Asp	Ser	Leu	Gly	Met	Ser	Lys	Lys	Thr	
582				20				_	25		_			30	_		
583 584	בות	Thr	Lve	λνα	Gln	7 ~~	Dro	λκα	uic	7 200	val	Dro	Tara	TIO	ח ז ת	The	
585	мта	1111	цу5 35	Arg	Gln	Arg	PIO	40	nis	Arg	val	PIO	பழக 45	TTE	AIA	IIII	
586																	
587	Leu		Ser	Thr	Ile	Arg		Cys	Arg	Ser	Leu		Ser	Ala	Cys	Asn	
588 589		50					55					60					
590	Leu	Ile	Ala	Leu	Ile	Leu	Ile	Leu	Leu	۷al	His	Lys	Ile	Ser	Ala	Ala	
591	65					70					75	-				80	
592 593	C111	7 an	Dho	~1.,	T 011	C1.,	Tlo	T 011	<i>α</i> 1	T1.	Com	7 ~ ~	The	7 ~~	Com	TT = -	
593 594	GIY	ASII	Pile	GIU	Leu 85	GIU	TTE	пеп	GIU	90	ser	ASII	1111	ASII	95	nis	
595																	
596	Leu	Leu	Asn		Tyr	Cys	Cys	Gly		Pro	Ala	Glu	Leu	-	Ala	Thr	
597 598				100					105					110			
599	Lys	Thr	Ile	Gly	Cys	Ser	Pro	Cys	Thr	Thr	Ala	Phe	Arg	Leu	Cys	Leu	
600			115					120					125				
601 602	Lve	Glu	Тиг	Gln	Thr	Thr	Glu	Gln	Glv	7.1 2	Sar	Tlo	Sar	Thr	Glv	Cve	
603	Бур	130	-y-	0111	1111	1111	135	OIII	OLY	Aια	ber	140	DCI	1111	Gry	Cys	
604																	
605	Ser 145	Phe	Gly	Asn	Ala	Thr 150	Thr	Lys	Ile	Leu		Gly	Ser	Ser	Phe		
606 607	145					150					155					160	
608	Leu	Ser	Asp	Pro	Gly	Val	Gly	Ala	Ile	Val	Leu	Pro	Phe	Thr	Phe	Arg	
609					165					170					175		
610 611	Tro	Thr	Lvs	Ser	Phe	Thr	Leu	IJe	Leu	G] n	Ala	Lev	Asp	Met	Tvr	Asn	
612			_, _	180					185					190	- I -		

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613																	
614	Thr	Ser	Tyr	Pro	Asp	Ala	Glu	Ara	Leu	Ile	Glu	Glu	Thr	Ser	Tvr	Ser	
615			195		-			200					205		-1-		
616	~-7			_	_	_	_		_		_				_	_	
617 618	GIY	Val 210	Ile	Leu	Pro	Ser		Glu	Trp	Lys	Thr		Asp	His	Ile	Gly	
619		210					215					220					•
620	Arq	Asn	Ala	Arq	Ile	Thr	Tyr	Arq	Val	Arq	Val	Gln	Cvs	Ala	Val	Thr	
621	225					230	•	_		,	235					240	
622				_	_												
623	Tyr	Tyr	Asn	Thr	Thr	Cys	Thr	Thr	Phe		Arg	Pro	Arg	Asp		Gln	
624 625					245					250					255		
626	Phe	Glv	His	Tvr	Ala	Cvs	Glv	Ser	Glu	Glv	Gln	Lvs	T.e.ii	Cvs	T.e.11	Δen	
627				260		· 1 ·	1		265		<b></b>			270		11011	
628																	
629	Gly	Trp		Gly	Val	Asn	Cys		Glu	Ala	Ile	Cys	Lys	Ala	Gly	Cys	
630			275					280					285				
631 632	7	Dwo	7707	774 ~	<b>a</b> 1												
633	Asp	290	Val	HIS	GTA												
634		200															
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636	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	10:5	:								
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650	CGG	rgga(	CTT (	CCTT	CGTGT	T A	rggto	GGA	G CCC	CTCGC	GAA	CGG	GGGT	raa (	CACTO	BAAAGG	60
651																	
652	TCG	AGTA	CCC A	ATTTC	CCGT	CA TA	AACGO	GTT	GT(	CGCC	CCCT	AGG	GTC	GGA (	STCA	GTGGA	120
653	aaa	77.00	naa 1		7000	a a	7007	7000		03 O3 0		Om 3			nn aa/	202.000	100
654 655	CGGG	JAGG.	ICG A	ACAA		اق فاد	AUDE		r GG.	I'ACA'	rGGT	GTA	AGGT	JTT :	racco	GACCG	180
656	GGC	AAAC	GG 1	CAC	ACCGZ	AA AC	GGGT	rgaac	G GG	CAACT	racg	GGG	rcgro	CT (	GCCC	STCCAT	240
657						••								· `			2.0
658	CGA	GTCT(	GGT A	AAGA	GGT	CG CC	CTTA	AG									267
659																	
660 661	(2)	INF	ORMAT	LION	FOR	SEQ	ID 1	10 : 6 :	:								
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664 665 666 667 668 669	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown  (ii) MOLECULE TYPE: cDNA	
671		
672		
673	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
674 675	GAATTCCTTC CATTATACGT GACTTTTCTG AAACTGTAGC CACCCTAGTG TCTCTAACTC	60
676	GAATICCTIC CATTATACGI GACTITICIG AAACIGIAGC CACCCIAGIG TCTCTAACIC	60
677	CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GCTCCTTAAT	120
678		
679	GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC	180
680	330000010	
681 682	AACCCGGAAC TGAAGGCTGG CTCTCACCCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG	240
683	TGTTAGATGT GAATGTCCGT GGCCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCCC	300
684	TOTALIST GRANDICCT GOCCHOMIC GCIGCACCC ATTOMICITY GCITCICC	300
685	GAGGAGGCAG CTCAGATTTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA	360
686		
687	TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGNC CAGACAGACC GGACTGGTGA	420
688		400
689 690	GATGGCCCTG CACCTTGCAG CCCGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA	480
691	TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCCGC TGTCCACTCC ATGCTGCAGT	540
692	Todioofodi diffodiano occidenti diffodoco fofodacio affortoadi	340
693	GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA	574
694		
695	(2) INFORMATION FOR SEQ ID NO:7:	
696	(*)	
697 698	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 295 base pairs	
699	(B) TYPE: nucleic acid	
700	(C) STRANDEDNESS: double	
701	(D) TOPOLOGY: unknown	
702		
703	(ii) MOLECULE TYPE: cDNA	
704		
705 706		
707	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
708	(NII) DIGOLAGI DIBONII IIONI DIG ID NO	
709	TCCAGATTCT GATTCGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA	60
710		
711	CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT	120
712 713	GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTCAC TGGGCAGCTG	180
714	GCCAAGCGGA IGIGAAIGCA GIGGAIGACC AIGGAAAAAIC IGCICIICAC IGGGCAGCIG	100

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715 716	CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTTGAAAAA TGGGGCCAAC CGAGACATGC	240
717	AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCG GGAGGAGCTA TAAGC	295
718		
719		
720	(2) INFORMATION FOR SEQ ID NO:8:	
721 722	(i) CECHENCE CUADACTEDICTICS.	
723	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 248 base pairs	
724	(B) TYPE: nucleic acid	
725	(C) STRANDEDNESS: double	
726	(D) TOPOLOGY: unknown	
727		
728	(ii) MOLECULE TYPE: cDNA	
729		
730		
731	/ '\	
732	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
733 734	GAATTCCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG	60
735	DELOGICATI CAGGAGGARA GAGGGGGGGGGGGGGGGGGGGGGGGGGG	60
736	ACTCGTTCCC AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA	120
737		
738	TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA	180
739		
740	GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG	240
741	CA CA COMO	0.40
742 743	CAGAGCTG	248
744	(2) INFORMATION FOR SEQ ID NO:9:	
745	(a) intoidiffication of the second of the se	
746	(i) SEQUENCE CHARACTERISTICS:	
747	(A) LENGTH: 323 base pairs	
748	(B) TYPE: nucleic acid	
749	(C) STRANDEDNESS: double	
750	(D) TOPOLOGY: unknown	
751 752	(ii) MOLEGIEE MYDE. ADNA	
752 753	(ii) MOLECULE TYPE: cDNA	
754		
755		
756		
757	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
758		
759	TACGTATCTC GAGCACAGAC AGCTGACGTA CACTTTTNNA GTGCGAGGGA CATTCGTCCG	60
760	ACCACHACCA ACAMMAACCA MOACMACCAM ACCACGAMCA CAAACAACAACAACAACAACAACAACAACAACAACAA	100
761 762	ACCAGTACGA ACATTTAGGC TCAGTACGGT AGGTCCATGG CCAAGACTAG GAGACGTAGG	120
763	GAGCTACAGG TCCCGCTCGC TAAACTCGGA CCACTGAAAC CTCCGGTCGA CAGTCGGTAA	180
764		
765	GCGAACAAGA GGGCCAGATC TTAGAGAAGG TGTCGCGGCG AGACTCGGGC TCGGGTCAGG	240

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

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CGGCCTTAAG GACGTCGGGC CCNNNAGGTG ATCAAGATCT CGNCNCGGCG GGCGCCACCT   300	766																	
769 CGAGGNCGAA AACAAGGGAA ATC  770 (2) INFORMATION FOR SEQ ID NO:10:  773 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 3234 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown  779 (ii) MOLECULE TYPE: cDNA  781 (ii) MOLECULE TYPE: cDNA  782 (iii) MOLECULE TYPE: cDNA  783 (iii) FEATURE: (B) LOCATION: 13234  784 (A) NAME/KEY: CDS (B) LOCATION: 13234  785 (B) LOCATION: 13234  786 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  787 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  789 (SG CAG GAG GAC GGG GGC AAC AAG GTC TGC AGC TGC AAC AAC AAC AAC AAC AAC AAC AAC AAC A		CGG	CCTT	AAG (	GACG'	TCGG	GC C	CNNN	AGGT	G AT	CAAG	ATCT	CGN	CNCG	GCG (	GCG	CCACC	T 300
772 (2) INFORMATION FOR SEQ ID NO:10:  773 (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 3234 base pairs  (B) TYPE: nucleic acid  777 (C) STRANDEDNESS: double  (778 (D) TOPOLOGY: unknown  780 (ii) MOLECULE TYPE: cDNA  781 (ix) FEATURE:  783 (ix) FEATURE:  784 (A) NAME/KEY: CDS  785 (B) LOCATION: 13234  786  787  788 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  789  790 TGC CAG GAG GAC GGG GAC AAC AAG GTC TGC AGC TGC AAC AAC AAC  791 (YES GIN Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Asn Phe Asn Asp  792 1 15  793  794 CAC GGG TGC GGC TGG GAC GGC GGT GAC TGC TCC TAAC TTC AAT GAC  795 His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp  796  797  798 CCC TGG AAG AAC TGC ACG CAG TCC TCTG CAG TGC AAG TAC TAC AAC  799 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser  790 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp  801  802 GAC GGC TTT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC  803 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp  804 50  805 60  806 GGC TTT GAC TGC CAG CGC GAG GGC CAG TGC AAC CCC CTG TAC GAC  807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asp Pro Leu Tyr Asp  808 65 70  70 75 80  809  800 CAG TAC TGC CAG GAC CAC TTC AGC GGC GGC CTC CTC CAC  801 Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys  801 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGC CAC TGC GAC CAC GGC TGC  803 Asp Gly Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys  809  801 CAG TAC TGC CAG GAG TGC GAC GGG CTC GAC CAG GGC TGC  803 Asp Gly Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys  801 AAC AGC GGG GAG TGC GAC GGG CTG GAC TGC GAC CAG GGC TGC  802 Ash Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val	769	CGA	GONC	GAA 2	AACA	AGGG	AA A	rc										323
(1)   SEQUENCE CHARACTERISTICS:																		
(i) SEQUENCE CHARACTERISTICS:   (a) LENGTH: 3234 base pairs	772	(2)	INF	ORMA'	LION	FOR	SEQ	ID 1	NO:1	0:								
Type: nucleic acid			(i	) SEC	OUEN	CE CI	TARAC	מידים:	TSTT	cs.								
777 (C) STRANDEDNESS: double (D) TOPOLOGY: unknown 778 (D) TOPOLOGY: unknown 779 780 (ii) MOLECULE TYPE: cDNA 781 782 783 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 13234 786 787 788 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: 789 790 TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC 791 Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn 792 1 5 10 15 793 794 CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC 795 His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp 796 20 25 30 797 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGC TAG TAC TAC TTC AGT 798 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGC TGC TAC TTC AGT 799 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser 800 35 40 45 801 802 GAC GGC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 803 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 804 50 6GC TTT GAC TGC CAG CGT GGG GAA GGC CAG TGC AAC CCC CTG TAC GAC 805 806 607 GGC TTT GAC TGC CAG CGT GGG GAA GGC CAG TGC AAC CCC CTG TAC GAC 807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 808 65 70 65 66 67 68 67 68 68 69 60 61 61 61 61 61 61 61 61 61 61 61 61 61	775		\-	()	A) L	ENGT	H: 32	234 ]	base	pai	rs							
778 (D) TOPOLOGY: unknown 779 780 (ii) MOLECULE TYPE: cDNA 781 782 783 (ix) FEATURE: 784 (A) NAME/KEY: CDS 785 (B) LOCATION: 13234 786 787 788 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: 788 789 790 TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC 791 Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn 792 1 5 10 793 794 CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC CTC AAC TTC AAT GAC 795 His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp 796 20 797 798 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGC AGC TTC AGC 797 798 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGC AGC TTC AGT 799 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser 790 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 790 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 790 Asp Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 798 Asp Gly Try Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 798 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGC CAC TGC GAC CAG GGC TGC 799 ASP Gly Try Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 790 Asp Gly Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 790 Asp Gly Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 790 Asp Gly Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 790 Asp Gly Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 790 Asp Gly Asp Cys Glu Try Asp Gly Leu Asp Cys Ala Glu His Val				•														
780 (ii) MOLECULE TYPE: cDNA 781 782 783 (ix) FEATURE: 784 (A) NAME/KEY: CDS 785 (B) LOCATION: 13234 786 787 788 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: 788 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: 789 TGC CAG GAG GAC GCG GGC AAC AAG GTC TCC AGC TGC AAC AAC CYS Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn 15 791 Cys Gln Glu Asp Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn 15 792 1 5 10 15 793 794 CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC 96 795 His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp 20 25 30 797 798 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC AAC TTC AGT 144 799 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser 40 801 A5 802 GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 192 803 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 50 805 GGC TTT GAC TGC CAG CGT GCC GAA GGC CAG TGC AAC CCC CTG TAC GAC 192 806 GGC TTT GAC TGC CAG CGT GCC GAA GGC CAG TGC AAC CCC CTG TAC GAC 240 807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 80 806 GGC TTT GAC TGC CAG CGT GCC GAA GGC CAG TGC AAC CCC CTG TAC GAC 240 807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 80 809 61 CAG TAC TGC AAG GAC CAC TTC AGC GAC GAC CAG GGC TGC CAG TGC										DIE								
781 782 783																		
782 783			(ii	) MO	LECU	LE T	YPE:	CDN	A									
784																		
785 786 787 788 789 789 790 790 790 790 790 790 790 790 790 79			(ix															
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788				()	J, L	JCAI.	1014.	<b></b>	3234									
789 790 790 790 790 790 790 791 791 792 793 794 790 792 793 794 796 797 798 799 799 799 799 799 799 790 790 790 790																		
790         TGC         CAG         GAG         GAC         GGC         GGC         AAC         AAG         GTC         TGC         AGC         CTG         CAG         TAC         AAC         AAG         GTC         CTG         CAG         TGC         AAC         AAC         AAG         GTC         CTG         CYS         Ser         Leu         GIN         CYS         ASN         ASN <td></td> <td></td> <td>(xi</td> <td>) SE</td> <td>QUEN</td> <td>CE DI</td> <td>ESCR:</td> <td>IPTI</td> <td>ON:</td> <td>SEQ :</td> <td>ID N</td> <td>0:10</td> <td>:</td> <td></td> <td></td> <td></td> <td></td> <td></td>			(xi	) SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID N	0:10	:					
792		TGC	CAG	GAG	GAC	GCG	GGC	AAC	AAG	GTC	TGC	AGC	CTG	CAG	TGC	AAC	AAC	48
793 794 CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC 795 His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp 796 797 798 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT 799 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser 800 801 802 GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 803 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 804 50 805 806 GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC CTC TTC GAC 807 808 808 609 810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GAC GGC CAG TGC CTC TTC AGC 809 810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGC CAG TGC CTC TTC AGC 811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG TGG GAC GGC CTG GAC TGT GCG GAG CAT GTA 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val			Gln	Glu	Asp		Gly	Asn	Lys	Val	Cys	Ser	Leu	Gln	Cys	Asn	Asn	
794 CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC 96 795 His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp 796 797 798 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT 144 799 Pro Trp Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser 800 801 802 GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 192 803 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 804 50 55 60 805 806 GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC 240 807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 808 65 70 70 75 80 809 810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC CTG 811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys Asp Gln Gly Cys Asp 812 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG TGC GAG TGC GAC GGC CTG TAC GAC CAG GAC CAT GTA Asp Cys Ala Glu His Val		1				5					10					15		
795         His Ala Cys Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp 796         20         25         25         30         <		CAC	GCG	TGC	GGC	TGG	GAC	GGC	GGT	GAC	TGC	TCC	CTC	AAC	TTC	AAT	GAC	96
797 798																		
798					20					25					30			
799         Pro         Trp         Lys         Asn         Cys         Thr         Gln         Ser         Leu         Gln         Cys         Trp         Lys         Tyr         Phe         Ser           801         35         40         40         45         45         45           801         GO         GAC         GGC         AGC         AGC         AGC         CGC         GGC         TTC         TTC         GAC         192           802         GAC         GGC         CAC         TGT         GAC         AGC         CAG         TGC         AAC         TCA         GCC         GGC         TTC         GAC         ASP         BAP         ASP         SSP         GGC         GAC         AGC         CAG         CAG         CAG         CAG         CAG         GGC         GAA         GGC         CAG         TGC         AAC         CCC         CTG         TAC         GAC         240           805         TTT         GAC         TGC         CAG         CGT         GCG         GAA         GGC         CAG         TGC         AAC         CCC         CTG         TAC         ASP         ASP         BO         AS		CCC	TGG	AAG	AAC	TGC	ACG	CAG	TCT	CTG	CAG	TGC	TGG	AAG	TAC	TTC	AGT	144
801 802 GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC 803 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 804 50 55 60 805 806 GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC 807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 808 65 70 75 80 809 810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC 811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA 836 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val																		
802       GAC       GGC       CAC       TGT       GAC       AGC       CAG       TGC       AAC       TCA       GCC       GGC       TGC       CTC       TTC       GAC       192         803       Asp       Gly       His       Cys       Asp       Ser       Gln       Cys       Asn       Ser       Ala       Gly       Cys       Leu       Phe       Asp         804       50       TTT       GAC       TGC       CAG       CGT       GCG       GAA       GGC       CAG       TGC       AAC       CCC       CTG       TAC       GAC       240         807       Gly       Phe       Asp       Cys       Gln       Arg       Ala       Glu       Gly       Gln       Cys       Asn       Pro       Leu       Tyr       Asp         808       65       TGC       CAG       CAC       TTC       AGC       GGC       GAC       GGC       TGC       CAC       TGC       Asp       Bo       80       80       80       80       80       80       80       80       80       80       80       80       80       80       80       80       80       80       80<				35					40					45				
803 Asp Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 804 50 55 60 55 60 60 805 805 806 GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC 240 807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 808 65 70 70 75 80 80 809 810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC 288 811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG GAC GGG CTG GAC TGC GAC GAC GAG GAG CAT GTA 336 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val		GAC	GGC	CAC	TGT	GAC	AGC	CAG	TGC	AAC	TCA	GCC	GGC	TGC	CTC	TTC	GAC	192
805 806																		
806 GGC TTT GAC TGC CAG CGT GCG GAA GGC CAG TGC AAC CCC CTG TAC GAC 807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 808 65 70 75 80 809 810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC 811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val			50					55					60					
807 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr Asp 808 65 70 70 75 80 80 809 810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC 288 811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG GGC TGC GAC AGC GGG CTG GAC AGC GGG CAC TGC GAC AGC GGG CAC TGC GAC AGC GGG CAC TGC GAC AGC GGG CAC AGC GGG CAC AGC GAC AGC AG		GGC	TTT	GAC	TGC	CAG	CGT	GCG	GAA	GGC	CAG	TGC	AAC	CCC	CTG	TAC	GAC	240
809 810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC 288 811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val																		
810 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC 811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val		65					70					75					80	
811 Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys 812 85 90 95 813 814 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val		CAG	TAC	TGC	AAG	GAC	CAC	ттс	AGC	GAC	GGG	CAC	тсс	GAC	CAG	GGC	TGC	288
813 814 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val																		200
814 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA 336 815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val			-	-	-	85				_	90		-	_		95		
815 Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala Glu His Val		дас	AGC	GCG	GAG	ፐርር	GAG	тсс	GAC	GGG	СТС	GAC	тст	GCG	GAG	СЪТ	СΤΣ	336
816 100 105 110																		330
	816				100					105					110			

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817	aaa	C A C	700	ama	000	000	000	7.00	ama	<b>ст</b> с	ama	СПС	ama	ama		aaa	
818 819					GCG Ala												384
820	PIO	GIU	115	ьeu	Ата	Ата	GIA	120	ьeu	vaı	vai	vaı		ьeu	мет	Pro	
821			113					120					125				
822	CCG	GVG.	CAG	СПС	CGC	777	7 CC	TICC	mma	az a	mm/c	ama	aaa	070	ama	700	420
823																	432
824	FIO	130	GIII	пеп	Arg	ASII	135	ser	Pile	urs	Pne		Arg	GIU	ьeu	ser	
825		130					133					140					
826	CGC	стс	СТС	CAC	ACC	מממ	CTC	CTC	ጥጥር	አአር	ССТ	GAC	CCN	CAC	ccc	CAC	400
827					Thr												480
828	145	vai	пси	111.5	1111	150	vaı	val	FIIC	цуз	155	Asp	нта	птъ	СТУ	160	
829	113					130					133					100	
830	CAG	ΔТС	ΔΤα	ጥጥር	CCC	тъс	ТΔС	GGC	CGC	GAG	CAC	GAG	СТС	CGC	አአር	CAC	528
831					Pro												320
832	0111				165	- 7 -	- 7 -	O <sub>T</sub> y	my	170	Gru	GIU	шси	Arg	175	1113	
833					103					1,0					1,5		
834	CCC	ATC	AAG	ССТ	GCC	GCC	GAG	GGC	TGG	GCC	GCA	ССТ	GAC	GCC	СТС	СТС	576
835					Ala												3,0
836			-10	180			014	O	185	1114	1114		TIOP	190	LCu	Dea	
837				-00					100					100			
838	GGC	CAG	GTG	AAG	GCC	TCG	CTG	CTC	CCT	GGT	GGC	AGC	GAG	GGT	GGG	CGG	624
839					Ala												
840	-		195	-4				200		1	2		205	1	1	3	
841																	
842	CGG	CGG	AGG	GAG	CTG	GAC	CCC	ATG	GAC	GTC	CGC	GGC	TCC	ATC	GTC	TAC	672
843					Leu												
844	_	210	_			-	215		_		_	220				1	
845																	
846	CTG	GAG	ATT	GAC	AAC	CGG	CAG	TGT	GTG	CAG	GCC	TCC	TCG	CAG	TGC	TTC	720
847	Leu	Glu	Ile	Asp	Asn	Arg	Gln	Cys	Val	Gln	Ala	Ser	Ser	Gln	Cys	Phe	
848	225					230		-			235				-	240	
849																	
850	CAG	AGT	GCC	ACC	GAC	GTG	GCC	GCA	TTC	CTG	GGA	GCG	CTC	GCC	TCG	CTG	768
851	Gln	Ser	Ala	Thr	Asp	Val	Ala	Ala	Phe	Leu	Gly	Ala	Leu	Ala	Ser	Leu	
852					245					250					255		
853																	
854	GGC	AGC	CTC	AAC	ATC	CCC	TAC	AAG	ATC	GAG	GCC	GTG	CAG	AGT	GAG	ACC	816
855	Gly	Ser	Leu	Asn	Ile	Pro	Tyr	Lys	Ile	Glu	Ala	Val	Gln	Ser	Glu	Thr	
856				260					265					270			
857																	
858					CCG												864
859	Val	Glu		Pro	Pro	Pro	Ala	Gln	Leu	His	Phe	Met	Tyr	Val	Ala	Ala	
860			275					280					285				
861																	
862					CTT												912
863	Ala		Phe	Val	Leu	Leu		Phe	Val	Gly	Cys		Val	Leu	Leu	Ser	
864		290					295					300					
865	<b></b> -																
866					CGG												960
867	Arg	Lys	Arg	Arg	Arg	Gin	His	GTA	GIn	Leu	Trp	Phe	Pro	GLu	GLY	Phe	

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868 869	305					310					315					320	
870 871 872 873		GTG Val															1008
874 875 876 877		TCC Ser															1056
878 879 880 881		GAC Asp															1104
882 883 884 885		TTC Phe 370															1152
886 887 888 889		GAC Asp															1200
890 891 892 893		ATG Met															1248
894 895 896 897		TGC Cys															1296
898 899 900 901		ATC Ile															1344
902 903 904 905	_	GAG Glu 450															1392
906 907 908 909		AGC Ser															1440
910 911 912 913		GCC Ala															1488
914 915 916 917		AGC Ser															1536
918	CAT	GCG	GCT	GTG	TCT	GCC	GAC	GCA	CAA	GGT	GTC	TTC	CAG	ATC	CTG	ATC	1584

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919 920 921	His	Ala	Ala 515	Val	Ser	Ala	Asp	Ala 520	Gln	Gly	Val	Phe	Gln 525	Ile	Leu	Ile	
922 923 924 925				GCC Ala													1632
926 927 928 929				CTG Leu													1680
930 931 932 933				TCA Ser													1728
934 935 936 937				CAC His 580													1776
938 939 940 941				AAG Lys													1824
942 943 944 945				CTG Leu													1872
946 947 948 949				CTG Leu													1920
950 951 952 953				CCG Pro													1968
954 955 956 957				CTG Leu 660													2016
958 959 960 961				CTG Leu													2064
962 963 964				TAC Tyr													2112
965 966 967 968 969				CCC Pro													2160

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970 971 972 973	GAC Asp								2208
974 975 976 977	CTG Leu								2256
978 979 980 981	CAT His								2304
982 983 984 985	TTC Phe 770								2352
986 987 988 989	GAC Asp								2400
990 991 992 993	ATG Met					 		 	2448
994 995 996 997	CCT Pro								2496
998 999 1000 1001	GGC Gly								2544
1002 1003 1004 1005	AGT Ser 850								2592
1006 1007 1008 1009	GTG Val								2640
1010 1011 1012 1013	CTG Leu								2688
1013 1014 1015 1016 1017	CAC His								2736
1017 1018 1019 1020	GGC Gly								2784

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1021																	
1022	ACC	CAG	CAG	GTG	CAG	CCA	CAA	אאכ	ттΔ	CAG	ΔТС	CAG	CAG	CAG	ממכ	CTG	2832
1023		Gln															2032
1024		930					935					940					
1025												2 - 0					
1026	CAG	CCA	GCA	AAC	ΔΤΟ	CAG	CAG	CAG	$C\Delta\Delta$	ACC	СТС	CAG	CCG	CCA	CCA	CCA	2880
1027		Pro															2000
1028	945	110	ALG	Abii	110	950	0111	GIII	GIII	Der	955	GIII	FIO	FIO	FIO	960	
1029	743					220					933					900	
1030	CCD	CCA	CAG	CCG	CAC	СФФ	ccc	CTC	אממ	<b>ጥ</b> ሮ እ	ממא	acc	NGC.	ccc	CAC	CTC	2928
1031		Pro															2320
1031	PIU	PIO	GIII	PIO	965	ьeu	GLY	vai	ser	970	Ата	Ата	Ser	GIY		ьeu	
1032					202					9/0					975		
	aaa	aaa	700	mma	ama	7 CM	~~~	C 7 C	000	7.00	an a	aar	a	СШС	070	aar	2076
1034		CGG															2976
1035	GIY	Arg	ser		ьeu	ser	GIY	GIU		ser	GIN	Ата	Asp		GIN	Pro	
1036				980					985					990			
1037																	
1038		GGC															3024
1039	Leu	Gly		Ser	Ser	Leu	Ala			Thr	IIe	Leu			GIu	Ser	
1040			995					1000	)				1005	5			
1041																	
1042		GCC															3072
1043	Pro	Ala		Pro	Thr	Ser			Ser	Ser	Leu			Pro	Val	Thr	
1044		1010	)				1019	5				1020	)				
1045																	
1046		GCC															3120
1047		Ala	Gln	Phe	Leu	Thr	Pro	Pro	Ser	Gln	His	Ser	Tyr	Ser	Ser	Pro	
1048	102	5				1030	)				1035	5				1040	
1049																	
1050		GAC															3168
1051	Val	Asp	Asn	Thr	Pro	Ser	His	Gln	Leu	Gln	Val	Pro	Val	Pro	Val	Met	
1052					1045	5				1050	)				1055	5	
1053																	
1054	GTA	ATG	ATC	CGA	TCT	TCG	GAT	CCT	TCT	AAA	GGC	TCA	TCA	ATT	TTG	ATC	3216
1055	Val	Met	Ile	Arg	Ser	Ser	Asp	Pro	Ser	Lys	Gly	Ser	Ser	Ile	Leu	Ile	
1056				1060	כ				1069	5				1070	)		
1057																	
1058	GAA	GCT	CCC	GAC	TCA	TGG											3234
1059	Glu	Ala	Pro	Asp	Ser	Trp											
1060			1079	5													
1061																	
1062																	
1063	(2)	INFO	ORMA!	rion	FOR	SEQ	ID 1	NO:1	L:								
1064																	
1065			(i) S	SEQUE	ENCE	CHAI	RACTI	ERIST	rics:	:							
1066					LEI						ds						
1067				(B)	TYI	PE: a	amino	ac:	id								
1068				(D)	TOI	POLO	3Υ: ι	ınkno	own								
1069																	
1070		( )	ii) N	OLE	CULE	TYPE	E: pi	rote:	in								
1071							_										

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1072		(:	xi) s	SEQUI	ENCE	DES	CRIP'	rion	: SE	Q ID	NO:	11:				
1073 1074 1075 1076	Cys 1	Gln	Glu	Asp	Ala 5	Gly	Asn	Lys	Val	Cys 10	Ser	Leu	Gln	Cys	Asn 15	Asn
1077 1078 1079	His	Ala	Cys	Gly 20	Trp	Asp	Gly	Gly	Asp 25	Cys	Ser	Leu	Asn	Phe 30	Asn	Asp
1080 1081 1082	Pro	Trp	Lys 35	Asn	Cys	Thr	Gln	Ser 40	Leu	Gln	Cys	Trp	Lys 45	Tyr	Phe	Ser
1083 1084 1085	Asp	Gly 50	His	Cys	Asp	Ser	Gln 55	Cys	Asn <sub>.</sub>	Ser	Ala	Gly 60	Cys	Leu	Phe	Asp
1086 1087 1088	65				Gln	70			_		- 75				-	80
1089 1090 1091			_		Asp 85					90		_	_		95	-
1092 1093 1094				100	Cys		_	_	105		_	_		110		
1095 1096 1097			115		Ala			120					125			
1098 1099 1100		130			Arg		135					140				
1101 1102 1103	145				Thr	150				_	155	_			_	160
1104 1105 1106					Pro 165	-	_			170					175	
1107 1108 1109				180	Ala			_	185				-	190		
1110 1111 1112			195					200		_	_		205	_	_	Arg
1113 1114 1115		210			Leu		215		_			220				-
1116 1117 1118	225				Asn	230					235					240
1119 1120 1121	Gln	Ser	Ala	Thr	Asp 245	Val	Ala	Ala	Phe	Leu 250	Gly	Ala	Leu	Ala	Ser 255	Leu
1122	Gly	Ser	Leu	Asn	Ile	Pro	Tyr	Lys	Ile	Glu	Ala	Val	Gln	Ser	Glu	Thr

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1123				260					265					270		
1124 1125	1701	C7.,	Dro	Dree	Dro	Dwo	77.	<b>71</b> 5	T 011	TT 4 ~	Dha	N/ - 4-	m	**- 7	7 J _	77-
1125	val	Glu	275	PIO	PIO	PIO	Ald	280	ьeu	HIS	Pne	Mec	-	vai	Ата	Ата
1127			2/5					200					285			
1127	λla	Ala	Dho	Wal.	T OII	T All	Dho	Dho	17a l	C1.,	Cara	~1.,	V-1	T 011	T 011	Cox
1129	AIG	290	FIIC	vai	пеи	пеп	295	FIIE	vaı	СТУ	Cys	_	val	Leu	Leu	ser
1130		290					233					300				
1131	Δνα	Lys	Δrα	Δrα	Δνα	Gln	Hie	Glv	Gl n	T.011	Trn	Dha	Dro	Glu	Clar	Dho
1132	305	шую	n. g	AL 9	n. a	310	111.5	Gry	GLII	пец	315	FIIC	PIO	GIU	GLY	320
1133	505					310					313					320
1134	Lvs	Val	Ser	G] 11	Δla	Ser	Lvs	Lvs	Lvs	Δrσ	Δra	Glu	Pro	T.e.u	Glv	Glu
1135	_, _		501	014	325	001	Lyb	<b></b> ,5	Lys	330	9	Oru	110	шси	335	Olu
1136										550					333	
1137	Asp	Ser	Val	Glv	Leu	Lvs	Pro	Leu	Lvs	Asn	Ala	Ser	Asp	Glv	Ala	Leu
1138				340		-1-			345					350		Lou
1139																
1140	Met	Asp	Asp	Asn	Gln	Asn	Glu	Trp	Glv	Asp	Glu	Asp	Leu	Glu	Thr	Lvs
1141			355					360	1				365			
1142																
1143	Lys	Phe	Arq	Phe	Glu	Glu	Pro	Val	Val	Leu	Pro	Asp	Leu	Asp	Asp	Gln
1144	-	370	_				375					380		-	•	
1145																
1146	Thr	Asp	His	Arg	Gln	Trp	Thr	Gln	Gln	His	Leu	Asp	Ala	Ala	Asp	Leu
1147	385	_		_		.390					395	-			_	400
1148																
1149	Arg	Met	Ser	Ala	Met	Ala	Pro	Thr	Pro	Pro	Gln	Gly	Glu	Val	Asp	Ala
1150					405					410					415	
1151																
1152	Asp	Cys	Met	Asp	Val	Asn	Val	Arg	Gly	Pro	Asp	Gly	Phe	Thr	Pro	Leu
1153				420					425	•				430		
1154																
1155	Met	Ile	Ala	Ser	Cys	Ser	Gly	Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu
1156			435					440					445			
1157																
1158 `	Glu	Glu	Glu	Asp	Ala	Pro		Val	Ile	Ser	Asp		Ile	Tyr	Gln	Gly
1159		450					455					460				
1160		_	_	1	_			_	_						_	
1161		Ser	Leu	His	Asn		Thr	Asp	Arg	Thr	_	GIu	Thr	Ala	Leu	
1162	465					470					475					480
1163	_			_	_	_	_	_	_			_	_	_	_	~-7
1164	ьeu	Ala	Ата	Arg		ser	Arg	ser	Asp		Ala	ьуs	Arg	Leu		GIu
1165					485					490					495	
1166	- נע	C.~~	7 7 ~	7.~~	חות	7. ~~	т1 ~	<b>~1</b>	7 ~	7 ~	Ma+	<b>01.</b>	7	шЪ	D	т о
1167	ΑΙΆ	Ser	ATA	_	ATA	ASII	тте	GIII	_	ASII	Met	стЛ	Arg		Pro	ьeu
1168				500					505					510		
1169 1170	ш: ~	Ala	λ] -	17n 1	C0~	777	7\ ~~	<b>71</b> -	@1 ~	C1	77-7	Dha	<b>~</b> 1∽	T1 ^	T cvv	т1 ^
1170	птр	MIG	515	vaı	ser.	ATG	нар	520	GTII	GTÀ	val	rne	525	тте	ьeu	тте
1172			713					J 2 ()					ن ع د			
1173	Ara	Asn	Ara	Δla	Thr	Agn	Len	Agn	Δla	Δrσ	Met	Hic	Δαη	Glv	Thr	Thr
,_	9	11011	9	TIL		7705	Lu	Hab	ALG	Ar 9	1.100	1113	Top	O T Y	TIIL	T 11T

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1174 1175		530					535					540				
1176	Pro	Leu	Ile	Leu	Ala	Ala	Arg	Leu	Ala	Val	Glu	Gly	Met	Leu	Glu	Asp
1177	545					550	Ť				555	-				560
1178	_		_	_	•		_		_			_	_	_		_
1179 1180	Leu	Ile	Asn	Ser		Ala	Asp	Val	Asn		Val	Asp	Asp	Leu	-	Lys
1181					565					570					575	
1182	Ser	Ala	Leu	His	Trp	Ala	Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val
1183				580	-				585				-	590		
1184		_	_	_	_				_				_			
1185	Val	Leu		Lys	Asn	Gly	Ala		Lys	Asp	Met	Gln		Asn	Arg	Glu
1186 1187			595					600					605			
1188	Glu	Thr	Pro	Leu	Phe	Leu	Ala	Ala	Ara	Glu	Glv	Ser	Tvr	Glu	Thr	Ala
1189		610					615		5		1	620	-1-			
1190																
1191	-	Val	Leu	Leu	Asp		Phe	Ala	Asn	Arg	-	Ile	Thr	Asp	His	
1192	625					630					635					640
1193 1194	Asp	Arg	Leu	Pro	Ara	Asp	Tle	Δla	Gln	Glu	Ara	Met	His	His	Asn	Tle
1195					645	1101			0	650	••••		****		655	
1196																
1197	Val	Arg	Leu		Asp	Glu	Tyr	Asn		Val	Arg	Ser	Pro		Leu	His
1198				660					665					670		
1199 1200	Cly	Ala	Dro	Tou	C111	Clv	Thr	Dro	Thr	Ton	802	Dro	Dro	T 011	Cara	Cor
1200	СТУ	Ата	675	Leu	СТУ	СТУ	1111	680	1111	Бец	Ser	PIO	685	Бец	Cys	Ser
1202			0.5													
1203	Pro	Asn	Gly	Tyr	Leu	Gly	Ser	Leu	Lys	Pro	Gly	Val	Gln	Gly	Lys	Lys
1204		690					695					700				
1205 1206	17a l	Arg	Tara	Dro	Cox	Cox	Tara	C1	T 011	חות	Crra	<b>~1</b>	Com	Trea	<b>~1</b>	ת הות
1200	705	Arg	гуѕ	PIO	261	710	пур	Gry	Leu	Ата	715	GLY	ser	гуѕ	GIU	720
1208																,
1209	Lys	Asp	Leu	Lys	Ala	Arg	Arg	Lys	Lys	Ser	Gln	Asp	Gly	Lys	Gly	Cys
1210					725					730					735	
1211	T 011	T 011	7 an	Cox	Cor	C1	Mot	T 011	Com	Dwo	1707	7	Com	T 011	<i>α</i> 1	Com
1212 1213	Leu	Leu	Asp	740	ser	GIY	Mec	ьeu	745	PIO	vaı	Asp	ser	750	GIU	ser
1214				, 10					, 13					, 50		
1215	Pro	His	Gly	Tyr	Leu	Ser	Asp	Val	Ala	Ser	Pro	Pro	Leu	Leu	Pro	Ser
1216			755					760					765			
1217	D	D1	<b>01</b> -	<b>~</b> 1	0	D	0	77 7	D	<b>.</b>	<b>3</b>	***	<b>T</b>	D	a i	N/ - 1:
1218 1219	Pro	Phe 770	GIN	GIn	ser	Pro	775	vaı	Pro	Leu	Asn	780	Leu	Pro	GIY	мет
1219		, , ,					, , 5					700				
1221	Pro	Asp	Thr	His	Leu	Gly	Ile	Gly	His	Leu	Asn	Val	Ala	Ala	Lys	Pro
1222	785	_				790		-			795				-	800
1223	~ 7				_	~ 7	~ 7	~7	~~	_	_		<b>5</b> 1	~ 7	1	~1
1224	GLu	Met	Ala	Ala	Leu	GГУ	GГУ	GГУ	GLY	Arg	Leu	Ala	Phe	Glu	Thr	GTA

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1225					805					810					815	
1226	D	D	7	<b>T</b>	<b>a</b>	*** =	<b>.</b>	B	**. 7		_	<b>~</b> 1	1	_	1	
1227 1228	Pro	Pro	Arg	ьеи 820	ser	HIS	ьeu	Pro	825	Ата	Ser	GIY	Thr		Thr	Val
1229				020					025					830		
1230	Leu	Gly	Ser	Ser	Ser	Glv	Glv	Ala	Leu	Asn	Phe	Thr	Val	Glv	Glv	Ser
1231		1	835			<b>4</b> -1	<u> </u>	840					845	017	<b>U</b>	501
1232																
1233	Thr	Ser	Leu	Asn	Gly	Gln	Cys	Glu	Trp	Leu	Ser	Arg	Leu	Gln	Ser	Gly
1234		850					855					860				_
1235																
1236		Val	Pro	Asn	Gln	_	Asn	Pro	Leu	Arg	-	Ser	Val	Ala	Pro	Gly
1237	865					870					875					880
1238	D	<b>T</b>	0	<b>6</b> 11	~1	27 -	D	<b>a</b>	<b>.</b> .	~1		<b>~</b> 1			~1	_
1239 1240	Pro	Leu	ser	Thr		Ата	Pro	ser	Leu		Hls	GTĀ	мет	vaı	-	Pro
1240					885					890					895	
1242	T.e.11	His	Ser	Ser	T.e.u	Δla	Δla	Ser	Δla	T.e.11	Ser	Gln	Mot	Mot	Sar	Tur
1243	шси	*****	501	900	<b>D</b> Cu	niu	nia	DCI	905	пси	DCI	GIII	Mec	910	DCI	1 Y L
1244									,,,,					,,,,		
1245	Gln	Gly	Leu	Pro	Ser	Thr	Arg	Leu	Ala	Thr	Gln	Pro	His	Leu	Val	Gln
1246		-	915				Ū	920					925			
1247																
1248	Thr	Gln	Gln	Val	Gln	Pro	Gln	Asn	Leu	Gln	Met	Gln	Gln	Gln	Asn	Leu
1249		930					935					940				
1250	~1	_		_		~7	~1	~7	~ 7	_	_	~ 7	_	_	_	_
1251		Pro	Ата	Asn	тте		Gin	GIn	GIn	Ser		GIn	Pro	Pro	Pro	
1252 1253	945					950					955					960
1254	Pro	Pro	Gln	Pro	His	Len	Glv	Val	Ser	Ser	Δla	Δla	Ser	Glv	Hig	T.e.11
1255			02		965	cu	<b>-</b> 1	val	JCI	970	mu	1114	001	O <sub>T</sub>	975	Lcu
1256																
1257	Gly	Arg	Ser	Phe	Leu	Ser	Gly	Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro
1258				980					985					990		
1259																
1260	Leu	Gly		Ser	Ser	Leu	Ala			Thr	Ile	Leu			Glu	Ser
1261			995					1000	)				100	5		
1262 1263	Dro	- ר מ	T 011	Dwo	Th w	Com	T 011	Dwo	Com	C 0 20	T 011	170 l	Dwo	Dwo	7707	mb w
1263	PIO	Ala 1010		Pro	THE	ser			ser	ser	ьeu			Pro	vaı	Thr
1265		1010	,				1019	•				1020	,			
1266	Δla	Ala	Gln	Phe	Len	Thr	Pro	Pro	Ser	Gln	His	Ser	Tvr	Ser	Ser	Pro
1267	1029					1030			~~=	~	1035		-1-	~~_	~~-	1040
1268																
1269	Val	Asp	Asn	Thr	Pro	Ser	His	Gln	Leu	Gln	Val	Pro	Val	Pro	Val	Met
1270		_			1049					105					1055	
1271																_
1272	Val	Met	Ile	_		Ser	Asp	Pro		_	Gly	Ser	Ser			Ile
1273				1060	ט				1069	•				1070	)	
1274	<b>~1.</b> .	- רת	Dwa	7 ~~	C ~ ~	Паса										
1275	GIU	Ala	FLO	Asp	ser	тrр										

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1276		1075												
1277 1278 1279	(2) INF	ORMATIO	N FOR SI	Q ID	NO:1	2:								
1280	(i	) SEQUE												
1281			LENGTH:				rs							
1282			TYPE: ni											
1283 1284			STRANDEI TOPOLOG											
1285		(D)	IOPOLOG.	: unx	IIOWII									
1286	(ii	) MOLEC	JLE TYPI	: cDN	A									
1287	·	,												
1288														
1289	(ix	) FEATU												
1290			NAME/KE											
1291		(B)	LOCATIO	1: 2	1972									
1292 1293														
1293	(xi	) SEQUE	VCE DESC	דיים דקי	ON·	SEO '	א מד	0.12						
1295	(322	, blgcl.	TOL DED.		011.	OLQ.	10 11	0.12	•					
1296	G GAG G	TG GAT	GTG TTA	GAT G	TG A	AT G	TC C	GT G	GC C	CA G	AT GO	GC TO	ЭC	46
1297	Glu V	al Asp	Val Leu	Asp V	al A	sn Va	al A	rg G	ly P	ro A	sp G	Ly C	ys	
1298	1		5				:	10				:	15	
1299														
1300		TTG AT										-	-	94
1301	Thr Pro	Leu Me		a Ser	Leu	Arg	_	GIY	Ser	Ser	Asp		Ser	
1302 1303			20				25					30		
1304	GAT GAA	GAT GA	A GAT GO	'A GAG	GAC	TCT	TCT	GCT	AAC	ATC	ATC	ACA	GAC	142
1305		Asp Gl												
1306	-	3	-		•	40					45		-	
1307														
1308		TAC CA												190
1309	Leu Val	Tyr Gl	n Gly Al	a Ser		Gln	Ala	Gln	Thr	_	Arg	Thr	Gly	
1310 1311		50			55					60				
1311	GAG ATG	GCC CT	י מאר רי	ጥ ርርል	GCC	CGC	ጥልሮ	тСΣ	CGG	сст	СУТ	сст	GCC	238
1313		Ala Le												230
1314	65			70			_1_		75					
1315														
1316		CTC CTC												286
1317		Leu Le		-	Ala	Asp	Ala		Ala	Gln	Asp	Asn		
1318	80		8	5				90					95	
1319 1320	CCC		א מייים מי	m com	CCN	CTTC	CCA	CCT	CAT	ccc	C 7 7	CCT	CTC	334
1321		TGT CC Cys Pro												334
1322	or, ary	Cyb FI	100	a		val	105	1.1.u	1.55		U.1.1	110	· 4.1	
1323			•											
1324	TTC CAG	ATT CT	G ATT CO	C AAC	CGA	GTA	ACT	GAT	CTA	GAT	GCC	AGG	ATG	382
1325	Phe Gln	Ile Le		g Asn	Arg		Thr	Asp	Leu	Asp	Ala	Arg	Met	
1326		11	5			120					125			

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1327																	
1328	AAT	GAT	GGT	ACT	ACA	CCC	CTG	ATC	CTG	GCT	GCC	CGC	CTG	GCT	GTG	GAG	430
1329	Asn	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala	Arg	Leu	Ala	Val	Glu	
1330			130					135					140				
1331																	
1332	GGA	ATG	GTG	GCA	GAA	CTG	ATC	AAC	TGC	CAA	GCG	GAT	GTG	AAT	GCA	GTG	478
1333	Gly	Met	Val	Ala	Glu	Leu	Ile	Asn	Cys	Gln	Ala	Asp	Val	Asn	Ala	Val	
1334		145					150					155					
1335																	
1336	GAT	GAC	CAT	GGA	AAA	TCT	GCT	CTT	CAC	TGG	GCA	GCT	GCT	GTC	AAT	AAT	526
1337	Asp	Asp	His	Gly	Lys	Ser	Ala	Leu	His	Trp	Ala	Ala	Ala	Val	Asn	Asn	
1338	160	_		_	_	165				_	170					175	
1339																	
1340	GTG	GAG	GCA	ACT	CTT	TTG	TTG	TTG	AAA	AAT	GGG	GCC	AAC	CGA	GAC	ATG	574
1341	Val	Glu	Ala	Thr	Leu	Leu	Leu	Leu	Lys	Asn	Gly	Ala	Asn	Arg	Asp	Met	
1342					180				-	185	-			-	190		
1343																	
1344	CAG	GAC	AAC	AAG	GAA	GAG	ACA	CCT	CTG	TTT	CTT	GCT	GCC	CGG	GAG	GGG	622
1345	Gln	Asp	Asn	Lys	Glu	Glu	Thr	Pro	Leu	Phe	Leu	Ala	Ala	Arq	Glu	Glv	
1346		•		195					200					205		•	
1347																	
1348	AGC	TAT	GAA	GCA	GCC	AAG	ATC	CTG	TTA	GAC	CAT	TTT	GCC	AAT	CGA	GAC	670
1349				Ala													
1350		•	210			•		215		-			220			-	
1351																	
1352	ATC	ACA	GAC	CAT	ATG	GAT	CGT	CTT	CCC	CGG	GAT	GTG	GCT	CGG	GAT	CGC	718
1353				His													. — .
1354		225	E				230			5	E	235		5	E	5	
1355																	
1356	ATG	CAC	CAT	GAC	ATT	GTG	CGC	CTT	CTG	GAT	GAA	TAC	ААТ	GTG	ACC	CCA	766
1357				Asp													
1358	240					245	5				250	-1-				255	
1359																	
1360	AGC	ССТ	CCA	GGC	ACC	GTG	TTG	ACT	тст	GCT	СТС	TCA	CCT	GTC	ATC	тст	814
1361				Gly													
1362				1	260					265					270	-7-	
1363															- / -		
1364	GGG	CCC	AAC	AGA	тст	TTC	CTC	AGC	CTG	AAG	CAC	ACC	CCA	ATG	GGC	AAG	862
1365				Arg													332
1366	<b>-</b> -1			275					280	-1-				285	<b>4-1</b>	-1-	
1367																	
1368	AAG	ጥርጥ	AGA	CGG	כככ	AGT	GCC	AAG	AGT	ACC	ATG	ССТ	ACT	AGC	СТС	ССТ	910
1369				Arg													3_0
1370	-,,		290	3		~ ~ -		295					300				
1371								_,,									
1372	AAC	СТТ	GCC	AAG	GAG	GCA	AAG	GAT	GCC	AAG	GGT	AGT	AGG	AGG	AAG	AAG	958
1373				Lys													200
1374		305		-10			310			_, _	1	315	3	3	-1-	-1-	
1375																	
1376	тст	СТС	AGT	GAG	AAG	GTC	CAA	СТС	тст	GAG	AGT	TCA	GTA	ACT	TTA	TCC	1006
1377				Glu													
			~ ~ -		-1-				~~-		~~-						

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1378	320					325					330					335	
1379	aam.	amm.	C D III	таа	CITE N	<b>CD</b> 2	mam	a a m	G2 G	7.00	m . m	amm	maa	a		2.02	
1380 1381		GTT Val															1054
1382	110	val	нор	Ser	340	GIU	Ser	FIU	1113	345	TYL	vai	SET	ASP	350	1111	
1383					0.10					313					330		
1384	TCC	TCT	CCA	ATG	ATT	ACA	TCC	CCT	GGG	ATC	TTA	CAG	GCC	TCA	CCC	AAC	1102
1385	Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	Ile	Leu	Gln	Ala	Ser	Pro	Asn	
1386				355					360					365			
1387	aam	3 ma		~~~		~~~	~~~	~~~	~~=	~~~	~~-	~	~				
1388		ATG															1150
1389 1390	Pro	Met	370	Ата	Thr	ALA	Ата	375	Pro	Ата	Pro	vaı	380	Ala	GIN	HIS	
1391			3/0		•			3/3					360				
1392	GCA	CTA	тст	ттт	тст	AAC	СТТ	САТ	GAA	ATG	CAG	ССТ	TTG	GCA	САТ	GGG	1198
1393		Leu															1170
1394		385					390					395				1	
1395																	
1396	GCC	AGC	ACT	GTG	CTT	CCC	TCA	GTG	AGC	CAG	TTG	CTA	TCC	CAC	CAC	CAC	1246
1397	Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Gln	Leu	Leu	Ser	His	His	His	
1398	400		•			405					410					415	
1399		ama		~~~	~~~		~~~		~~=	~~-				- ~ ~		~	
1400		GTG															1294
1401 1402	тте	Val	ser	Pro	420	ser	GIA	ser	Ата	_	ser	ьeu	ser	Arg		HIS	
1402					420					425					430		
1404	CCA	GTC	CCA	GTC	CCA	GCA	СУТ	тсс	ΣΤС	ממכ	CGC	ΔТС	GAG	стс	ייעמ	GAG	1342
1405		Val															1312
1406				435			<u>-</u> -		440		3			445			
1407																	
1408	ACC	CAG	TAC	AAT	GAG	ATG	TTT	GGT	ATG	GTC	CTG	GCT	CCA	GCT	GAG	GGC	1390
1409	Thr	Gln	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu	Ala	${\tt Pro}$	Ala	Glu	Gly	
1410			450					455					460				
1411																	
1412		CAT															1438
1413	Thr	His	Pro	GIĀ	ile	Ата		GIn	ser	Arg	Pro		GIu	GIY	ьуs	His	
1414 1415		465					470					475					
1416	מדמ	ACC	ACC	ССТ	CGG	GAG	כככ	ጥጥር	CCC	כככ	אַדית	стс	ΔСТ	ጥጥር	CAG	СТС	1486
1417		Thr													-		1400
1418	480				5	485					490					495	
1419																	
1420	ATC	CCT	AAA	GGC	AGT	ATT	GCC	CAA	CCA	GCG	GGG	GCT	CCC	CAG	CCT	CAG	1534
1421	Ile	Pro	Lys	Gly	Ser	Ile	Ala	Gln	Pro	Ala	Gly	Ala	${\tt Pro}$	Gln	Pro	Gln	
1422					500					505					510		
1423																	
1424		ACC															1582
1425	ser	Thr	Cys		Pro	Ala	vaı	ALA	_	Pro	ьeu	Pro	Thr		Tyr	GIN	•
1426 1427				515					520					525			
1427	Δππ	CCA	GAD	ΔТС	GCC	ССТ	ጥጥር፤	כככ	ልርጥ	стс	сст	ጥጥር	כככ	ΔСΤ	פכר	ΔͲር	1630
1120		CCA	0.111	1110		001	-10		AGI	010	U - 1	110		AC 1	300	.110	1030

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1429	Ile	Pro	Glu	Met	Ala	Ara	Leu	Pro	Ser	Val	Ala	Phe	Pro	Thr	Ala	Met	
1430			530			5		535					540				
1431																	
1432			CAG														1678
1433	Met		Gln	Gln	Asp	Gly		Val	Ala	Gln	Thr		Leu	Pro	Ala	Tyr	
1434		545					550					555					
1435 1436	CMT	CCT	TTC	CCA	ccc	TICT.	CTC	ccc	770	TIN C	aaa	7 (7 7	aaa	CCT	TIC N	CAC	1726
1437			Phe														1726
1438	560	FIU	FIIC	FIO	AIG	565	vai	Сту	цуз	ıyı	570	1111	PIO	PIO	Ser	575	
1439	500					505					370					373	
1440	CAC	AGT	TAT	GCT	TCC	TCA	AAT	GCT	GCT	GAG	CGA	ACA	CCC	AGT	CAC	AGT	1774
1441			Tyr														
1442			•		580					585	J				590		
1443																	
1444	GGT	CAC	CTC	CAG	GGT	GAG	CAT	CCC	TAC	CTG	ACA	CCA	TCC	CCA	GAG	TCT	1822
1445	Gly	His	Leu	${\tt Gln}$	Gly	Glu	His	Pro	Tyr	Leu	Thr	Pro	Ser	Pro	Glu	Ser	
1446				595					600					605			
1447																	
1448			CAG														1870
1449	Pro	Asp	Gln	Trp	Ser	Ser	Ser		Pro	His	Ser	Ala		Asp	Trp	Ser	
1450			610					615					620				
1451	CAT	CITIC	700	700	700	CCT	700	aam	aaa	COM	COM	CC 7	CC 7	COM	C T C	aaa	1010
1452 1453			ACC Thr														1918
1454	Asp	625	1111	1111	ser	PIO	630	PIO	GIY	GTÅ	Ата	635	GTÅ	GTÅ	GIII	Arg	
1455		025					0.50					055					
1456	GGA	ССТ	GGG	ACA	CAC	ATG	тст	GAG	CCA	CCA	CAC	AAC	AAC	ATG	CAG	GTT	1966
1457			Gly														
1458	640					645					650					655	
1459																	
1460	TAT	GCG	TGA	GAGA(	GTC (	CACC	CCA	GT G	raga(	GACA:	C AAC	CTGA	CTTT	TGT	TAA	GCT	2022
1461	Tyr	Ala															
1462																	
1463																	
1464	GCT	3AGG/	AAC A	TAAP	GAAG(	ST C	ATCC	GGA(	G AGA	TAA	BAAG	AAA:	rctc:	rgg <i>i</i>	AGCC	AGCTTC	2082
1465					. ~										~	~~~~	0.4.0
1466	TAG	AGGTZ	AGG A	AAAG	AGAA	JA TO	3'I"I'C'.	l"TAT".	r cac	3ATA	ATGC	AAG	AGAA	3CA A	ATTCC	GTCAGT	2142
1467	mma	amaa	70m 1	N CO CO	70776	ים מי	nm v mc	n ~ x mr	n ame	00003	mam	מח א א		777 /	mmmz	TITICO N	2202
1468 1469	TTC	ACTGO	SGT A	ATCT	3CAA(	3G C.	LIAI.	IGAT.	L AT.	ICIA	ATCT	AATA	AAGA	JAA (	5111(	GTGGAA	2202
1470	አ ፕርር	מאמי	ነጥር 7	እ <b>ጥ</b> ፖለ	מא א כני	יירוי ייטיר	רמממי	ויכיכיאי	ר כיתיי	רידי א כיר	ירייירי	ጥጥረ፣	ה של להלהי	raa 1	אמאאי	raagat	2262
1471	AIG		11.0 1	-WIW	יהתטיי	-C I.		LCCM.	. G1.	LIAC.		110.	.AII.	.GG A	·GAM.	LACAI	2202
1472	GGA	rgctr	rat r	rgaad	GCCC	AG AG	CATTO	TTCC	AGC	ттас	ACT	GCA	ידינידין	AAG (	CCTC	GCAGGC	2322
1473				•			<b>-</b>						·		\		
1474	TTC	rgcc <i>i</i>	ATA :	rcca:	rgag <i>i</i>	AA GA	ATTC:	raca	TAC	CGT	CCTG	TTG	GAA:	TA :	rgcco	CTGGAA	2382
1475																	
1476	TTC	rgcc:	rga 2	ATTG	ACCT	AC GO	CATC	CCT	CTC	CCTT	GAC	ATTO	CTTT	rgt (	CTTC	ATTTGG	2442
1477																	
1478	TGC:	TTTT	GGT :	rttg	CACC	C TO	CCGT	TTAE	TAC	3CCC	CACC	AGC	ATGT	CAT A	AGGG	CAAGAC	2502
1479																	

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DATE: 12/16/93 TIME: 13:10:49

1480 CTTTGTGCTT TTGATCATTC TGGCCCATGA AAGCAACTTT GGTCTCCTTT CCCCTCGTT 1481 1482 CTTCCCGGTA TCCCTTGGAG TCTCACAAGG TTTACTTTGG TATGGTTCTC AGCACAAACC 2622 1483 1484 TTTCAAGTAT GTTGTTTCTT TGGAAAATGG ACATACTGTA TTGTGTTCC CTGCATATAT 2682 1485 CATTCCTGGA GAGAGAGGG GAGAAGAATA CTTTTCTTCA ACAAATTTTG GGGGCAGGAG 2742 1487 1488 ACCCTTCAA GAGGCTGCAC CTTAATTTT CTTGTCTTGT
1483 1484 TTTCAAGTAT GTTGTTTCTT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT 2682 1485 1486 CATTCCTGGA GAGAGAAGGG GAGAGAATA CTTTTCTTCA ACAAATTTTG GGGGCAGGAG 2742 1487 1488 ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT 2802 1489 TTACCAGGAA GAAGGGTGTA AGTTTGTTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTAAA 2862 1491 1492 GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTTAAAA CCAGAAAAAG 2922 1493 GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC 2982 1495 CACAGGTCCC CCTACTTCCT GCCAAGCAAT CCATTGACTG CCTGTATGGA ACACATTTGT 3042 1497 CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCAC CAGCATATGA AACTAGTCTT 3102 1499 AACTGTTGAG CCTTTCCTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG 3162 1500 CCATTTAGGA CTGAACTTC CTTAGCCCAA GGGACCCAGT GACAGTTGT TTCCGTTTGT 3222 1503 CAGATGATCA GTCTCACTG ATTATCTTC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1504 CACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAC GAAAACAGC 3342 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 TTATATGTTC AAGTGCAGA ATTGGAAAGT TGGACTTGT TCTCACTGAA GACATGGACT 3342 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TCTCACTGAA GACATGGACT 3342 1509 TCACACCGTG TGGTCCGTGT TACTGGAAACTT TCCAGTGAA GACATGGACT 3402 1509 TCACACCGTG TGGACAAAA GAGGAACTAT ATAGCAGCC TTGCTATTT CTGCTACCAT 3462 1501 TCATTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACAGGA AACTCAACAG 3522 1503 AACATTTCC TTTCCTAGAG TCACCTTTA GAGGATTATT GTGCTACCAT 3462 1501 AACATTTCC TTTCCTAGAG TCACCTTTA GAGGATAAACAGCC TTACCTACA GACTACCACA GACACTATA GACATTCCCA GACACTATA GACATTCCCA 3582 1514 AACATTTCC TTTCCTAGAG TCACCTTTA GATGATAATG GACAACTATA GACTGCCA 3582 1515 TTGTTCAGAC TGATTGCCC TCACCTGAAT CCACTCTCT TATTCATGCT CTTGGCAATT GACCTTCTA GACTTCCAC TTTGCTACA GACACTATA GACTTGCCA 3582 1516 TTGTTCAGAC TGATTGCCC TCACCTGAAT CCACTCTCT TATTCATGCT CTTGGCAATT GACCTTCTA GACTTCCAT 3582
1484         TTTCAAGTAT GTTGTTTCTT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT         2682           1486         CATTCCTGGA GAGAGAGGG GAGAAGAATA CTTTCTTCA ACAAATTTTG GGGGCAGGAG 2742           1487         ATCCCTTCAA GAGGCTGCAC CTTAATTTT CTTGTCTGT TGCAGGTCTT CATATAAACT 2802           1489         TTACCAGGAA GAAGGGTGTG AGTTTGTTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTAAA 2862           1491         GTTTTATCCT TGATAGTCTA GTTACTATGA CCCCCCCCC TTTTTTAAAA CCAGAAAAAG 2922           1493         GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC 2982           1495         CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT 3042           1496         CACAGGTCCC CCTACTTCCT GCCAAGCATT CCACTCACC CAGCATATGA AACTAGTCTT 3102           1497         CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT 3102           1498         CCCAGGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT 3102           1499         AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG 3162           1501         CAGATGATCA GTCCACTTCCTT CATACCCCA GAGGACCCAGT GACAGTTGC TCCCGTTTGT 3222           1503         CAGATGATCA GTCCTACTG ATTACTTCC CTTACCACA GAGCCCCAGT GACAGTTGC TCCCGTTTTCTT 3282           1504         CAGATGATCA GTCCACTGATACTG ATTACTTTC TCCACTACAG GCCCTGCCC AATCTTTCT TCCCTTTTCTT TCCCTTTCTT TCCTGTACAGT TCCACTACTAGACTTCTTCTTTCTTTCTTCTTCTTCTTCTTCTTTCT
1485 1486 CATTCCTGGA GAGAGAGGG GAGAAGAATA CTTTTCTTCA ACAAATTTTG GGGGCAGGAG 2742 1487 1488 ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT 2802 1489 TTACCAGGAA GAAGGGTGTG AGTTTGTTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTAAA 2862 1491 1492 GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTTAAAA CCAGAAAAAG 2922 1493 GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC 2982 1495 CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT 3042 1497 CCCAGATCTG AGCATTCTAG GCCTGTTCA CTCACTCAC CAGCATATGA AACTAGTCTT 3102 1499 AACTGTTGAG CCTTTCCTT CATATCCACA GAAGACACT TCTCAAATGT TGTACCCTTG 3162 1500 CACATTTAGGA CTGAACTTTC CTTAGCCCAA GGGACCCAG GACAGTTGC TTCCGTTTGT 3222 1501 CAGATGATCA GTCTCTACTG ATTATCTTCC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1506 TCACACCGTG TGGTCCGTG TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 TATATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGT TCCACTGAA GACATGGACT 3342 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGT TCCACTGAA GACATGGACT 3342 1509 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 TTCTTTCCT CTGAAGCGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1511 AACATTTCC TTTCCTAGAG TCACCTTTAA GACGACCT TTGCTATTTT CTGCTACCAT 3462 1512 TTCTTTCCT CTGAAGCGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 AACATTTCC TTTCCTAGAG TCACCTTTAA GACGACCT TTGCTATTTT CTGCTACCAT 3462 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CACCTTCTG TATTCATGCT CTTGGCAATT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 TTCTTTCCT CTGAAGCGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACCTCTCT TATTCATGCT CTTGGCAATT 3642
1486         CATTCCTGGA         GAGAGAAGGG         GAGAGAATA         CTTTCTTCA         ACAAATTTTG         GGGGCAGGAG         2742           1487         ACCCTTCAA         GAGGCTGCAC         CTTAATTTT         CTTGTCTGTG         TGCAGGTCT         CATATAAACT         2802           1489         TTACCAGGAA         GAAGGGTGTG         AGTTTGTTGT         TTTTCTGTGT         ATGGGCCTGG         TCAGTGTAAA         2862           1491         GTTTTATCCT         TGATAGTCTA         GTTACCTACC         TTTTTTAAAA         CCAGAAAAAG         2922           1493         GTTTGGAATG         TTGGAATGAC         CAAGAGACAA         GTTAACTCGT         GCAAGAGCCA         GTTACCCACC         2982           1495         CACAGGTCCC         CCTACTTCCT         GCCAAGCATT         CCATTGACTG         GCTGTATGGA         ACACATTTGT         3042           1497         CCCAGATCTG         AGCATTCTAG         GCCTGTTTCA         CTCACCTCC         CAGCATATGA         ACACATTTGT         3102           1498         CCCAGATCTG         ACCTTCCTT         CATATCCACA         GAAGACACTG         TCTCAAATGT         TGTACCCTTG         3162           1501         AACTGTTAGGA         CTGAACCTTC         CTTAGCCAA         GAGACCAGT         GCCAGGTTGCC         AATCTTTCTT         3282
1487 1488 ATCCCTTCAA GAGGCTGCAC CTTAATTTT CTTGTCTGTG TGCAGGTCTT CATATAAACT 2802 1489 1490 TTACCAGGAA GAAGGGTGTG AGTTTGTTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTAAA 2862 1491 1492 GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCAC TTTTTTAAAA CCAGAAAAAG 2922 1493 1494 GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCA GTTACCCACC 2982 1495 1496 CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT 3042 1497 1498 CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCAATAGA AACTAGTCTT 3102 1499 AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACG TCTCAAAATGT TGTACCCTTG 3162 1500 AACTGTTGAG CTGAACTTC CTTAGCCCAA GGGACCCAGT GACAGTTGT TGTACCCTTG 3162 1501 CCATTTAGGA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1504 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 1508 TTATATGTTC AAGTGCAGA ATTGGAAAGT TGGACTTGTT TCTCACTGAA GACATGGACT 3462 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCC TTGCTATTTT CTGCTACCAT 3462 1511 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1512 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1514 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 TTGTTCAGAC TGATTGCCC TCACCTGAAT CCACCTCTCT TATTCATGCT CTTGGCAATT 3642
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1489 1490 TTACCAGGAA GAAGGGTGTG AGTTTGTTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTAAA 2862 1491 1492 GTTTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTTTAAAA CCAGAAAAAG 2922 1493 1494 GTTTGGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC 2982 1495 1496 CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT 3042 1497 1498 CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT 3102 1499 1500 AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG 3162 1501 1502 CCATTTAGGA CTGAACTTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 3222 1503 1504 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 1508 TTATATGTTC AAGTGCAGA ATTGGAAAGT TGGACTTGTT TCTCACTGAA GACATGGACT 3462 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCC TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACACTATA GACTTGCTCA 3582 1515 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3582 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 35642
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1496 CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTTGT 1497 1498 CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT 1499 1500 AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG 1501 CCATTTAGGA CTGAACTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 1502 CCATTTAGGA CTGAACTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 1503 1504 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 1505 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 1507 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 1513 1514 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 1515 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 1517
1497 1498 CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT 3102 1499 1500 AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG 3162 1501
1499 1500 AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG 3162 1501 1502 CCATTTAGGA CTGAACTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 3222 1503 1504 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1505 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642
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1501 1502 CCATTTAGGA CTGAACTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 3222 1503 1504 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1505 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642
1502 CCATTTAGGA CTGAACTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT 3222 1503 1504 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1505 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642
1503 1504 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1505 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1504 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT 3282 1505 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642
1505 1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 3342 1507 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1506 TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT 1507 1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1508 TTATATGTTC AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC 3402 1509 1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 3462 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1510 CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT 1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 1515 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 1517
1511 1512 TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1512 TTCTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG 3522 1513 1514 AACATTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1513 1514 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA 3582 1515 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1515 1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1516 TTGTTCAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT 3642 1517
1517
1518 TCTTTGACTT TCTTTTAAGG GCAGAAGCAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT 3702
1519 1520 CTTCCTCTTC TCCTTGGGCC AGTTAATAAT TGGTCCATGG CTACACTGCA ACTTCCGTCC 3762
1521
1522 AGTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTTCTGC CTGGGCATTT TGTAGATATT 3822
1523
1524 AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCCTT CTATGGCTGC 3882
1525
1526 AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC 3942 1527
1528 CCTGCGTGTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCTAT CCAAATTTAT 4002
1529
1530 TGAACCAACA AAAATAATTA CTTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC 4062

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1531		
1532	GCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATT	r 4122
1533		
1534	IATCATTCTA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA	4182
1535		
1536	ACCTATCTGC ATGGACCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGT	4242
1537		
1538	GCGATGGCGA TGACTTTCTT CCCCTG	4268
1539		
1540	(a) THEODICETON FOR ONE TO NO. 12	
1541	(2) INFORMATION FOR SEQ ID NO:13:	
1542 1543	(i) SEQUENCE CHARACTERISTICS:	
1544	(A) LENGTH: 657 amino acids	
1545	(B) TYPE: amino acid	
1546	(D) TOPOLOGY: unknown	
1547	(5) 10102011 (1111101111	
1548	(ii) MOLECULE TYPE: protein	
1549	, , , , , , , , , , , , , , , , , , ,	
1550	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
1551		
1552	Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys Thr	
1553	1 5 10 15	
1554		
1555	Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser Asp	
1556	20 25 30	
1557		
1558	Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp Leu	
1559	35 40 45	
1560 1561	Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly Glu	
1562	50 55 60	
1563	33 00	
1564	Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala Lys	
1565	65 70 75 80	
1566		
1567	Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met Gly	
1568	85	
1569		
1570	Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val Phe	
1571	100 105 110	
1572		
1573	Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met Asn	
1574	115 120 125	
1575 1576	Agn Cly Thr Thr Dro Iou Ilo Iou Ala Ala Ara Iou Ala Val Clu Clu	
1576	Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly 130 135 140	
1578	720 733 740	
1579	Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp	
1580	145 150 155 160	
1581	====	

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1582 1583 1584	Asp	His	Gly	Lys	Ser 165	Ala	Leu	His	Trp	Ala 170	Ala	Ala	Val	Asn	Asn 175	Val
1585 1586 1587	Glu	Ala	Thr	Leu 180	Leu	Leu	Leu	Lys	Asn 185	Gly	Ala	Asn	Arg	Asp 190	Met	Gln
1588 1589 1590	Asp	Asn	Lys 195	Glu	Glu	Thr	Pro	Leu 200	Phe	Leu	Ala	Ala	Arg 205	Glu	Gly	Ser
1591 1592 1593	Tyr	Glu 210	Ala	Ala	Lys	Ile	Leu 215	Leu	Asp	His	Phe	Ala 220	Asn	Arg	Asp	Ile
1594 1595 1596	Thr 225	Asp	His	Met	Asp	Arg 230	Leu	Pro	Arg	Asp	Val 235	Ala	Arg	Asp	Arg	Met 240
1597 1598 1599		His	_		245				_	250	-				255	
1600 1601 1602		Pro	_	260					265					270	_	-
1603 1604 1605		Asn	275					280	-				285	-	-	-
1606 1607 1608		Arg 290					295					300				
1609 1610 1611	305	Ala	_			310	_		_		315			_	-	320
1612 1613 1614		Ser		_	325					330					335	
1615 1616 1617		Asp		340					345					350		
1618 1619 1620		Pro	355					360					365			
1621 1622 1623		Leu 370					375					380				
1624 1625 1626	385	Ser				390					395				_	400
1627 1628 1629		Thr			405					410					415	
1630 1631 1632	Val	Ser	Pro	Gly 420	Ser	GLY	Ser	Ala	Gly 425	Ser	Leu	Ser	Arg	Leu 430	His	Pro

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1633 1634 1635	Val	Pro	Val 435	Pro	Ala	Asp	Trp	Met 440	Asn	Arg	Met	Glu	Val 445	Asn	Glu	Thr
1636 1637 1638	Gln	Tyr 450	Asn	Glu	Met	Phe	Gly 455	Met	Val	Leu	Ala	Pro 460	Ala	Glu	Ġĺy	Thr
1639 1640 1641	His 465	Pro	Gly	Ile	Ala	Pro 470	Gln	Ser	Arg	Pro	Pro 475	Glu	Gly	Lys	His	Ile 480
1642 1643 1644	Thr	Thr	Pro	Arg	Glu 485	Pro	Leu	Pro	Pro	Ile 490	Val	Thr	Phe	Gln	Leu 495	Ile
1645 1646 1647	Pro	Lys	Gly	Ser 500	Ile	Ala	Gln	Pro	Ala 505	Gly	Ala	Pro	Gln	Pro 510	Gln	Ser
1648 1649 1650	Thr	Cys	Pro 515	Pro	Ala	Val	Ala	Gly 520	Pro	Leu	Pro	Thr	Met 525	Tyr	Gln	Ile
1651 1652 1653	Pro	Glu 530	Met	Ala	Arg	Leu	Pro 535	Ser	Val	Ala	Phe	Pro 540	Thr	Ala	Met	Met
1654 1655 1656	Pro 545	Gln	Gln	Asp	Gly	Gln 550	Val	Ala	Gln	Thr	Ile 555	Leu	Pro	Ala	Tyr	His 560
1657 1658 1659	Pro	Phe	Pro	Ala	Ser 565	Val	Gly	Lys	Tyr	Pro 570	Thr	Pro	Pro	Ser	Gln 575	His
1660 1661 1662	Ser	Tyr	Ala	Ser 580	Ser	Asn	Ala	Ala	Glu 585	Arg	Thr	Pro	Ser	His 590	Ser	Gly
1663 1664 1665	His	Leu	Gln 595	Gly	Glu	His	Pro	Tyr 600	Leu	Thr	Pro	Ser	Pro 605	Glu	Ser	Pro
1666 1667 1668	Asp	Gln 610	Trp	Ser	Ser	Ser	Ser 615	Pro	His	Ser	Ala	Ser 620	Asp	Trp	Ser	Asp
1669 1670 1671	Val 625	Thr	Thr	Ser	Pro	Thr 630	Pro	Gly	Gly	Ala	Gly 635	Gly	Gly	Gln	Arg	Gly 640
1672 1673 1674	Pro	Gly	Thr	His	Met 645	Ser	Glu	Pro	Pro	His 650	Asn	Asn	Met	Gln	Val 655	Tyr
1675 1676 1677	Ala															
1678 1679 1680	(2)				FOR											
1681 1682 1683			( Z	A) LI 3) T	ENGTI /PE :   RANI	H: 77 amir	7 ami	ino a	acids	3						

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1684			(D)	TOI	POLO	GΥ: ι	ınkno	own									
1685																	
1686		(ii)	MOLI	ECULI	E TY	PE: ]	pept:	Lde									
1687																	
1688																	
1689																	
1690		(xi)	SEQU	JENCI	E DES	SCRI	PTIO	1: SI	EQ II	O. NO	:14:						
1691		_		_					_								
1692			Asp	Ile	Asp		Cys	Asp	Gln	Gly		Pro	Cys	Glu	His		Gly
1693		1				5					10					15	
1694					_		_		_	_	_	_	_	_	_		
1695		Ile	Cys	Va⊥		Thr	Pro	GLy	Ser		Arg	Cys	Asn	Cys		Gln	Gly
1696					20					25					30		
1697		_	_	_				_	_		_		_		_		
1698		Phe	Thr		Pro	Arg	Cys	Glu		Asn	Ile	Asn	Glu	Cys	Glu	Ser	His
1699				35					40					45			
1700																	
1701		Pro	Cys	Gln	Asn	Glu	Gly	Ser	Cys	Leu	Asp	Asp	Pro	Gly	Thr	Phe	Arg
1702			50					55					60				
1703							_			_		_		_			
1704		_	Val	Cys	Met	Pro	Gly	Phe	Thr	Gly	Thr	Gln	Cys	Glu			
1705		65					70					75					
1706																	
1707	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:15	:								
1708																	
1709		(i)	SEQU														
1710				LEI					cids								
1711			(B)	TYI	PE: 8	amino	ac:	id									
1712			(C)	STI	RANDI	EDNE	SS: 8	sing	le								
1713			(D)	TOI	POTO(	GΥ: ι	ınkno	own									
1714																	
1715		(ii)	MOLI	ECULI	E TY	PE: ]	pept:	Lde									
1716																	
1717																	
1718																	
1719		(xi)	SEQ	JENCI	E DE	SCRI	PTIO	1: SI	EQ II	ON C	:15:						
1720				_							_				<b>-</b>		<b>-</b>
1721		Asn	Asp	Val	Asp	Glu	Cys	Ser	Leu	Gly	Ala	Asn	Pro	Cys	Glu		Gly
1722		1				5					10					15	
1723												_					_
1724		Gly	Arg	Cys	Thr	Asn	Thr	Leu	Gly	Ser	Phe	Gln	Cys	Asn	Cys	Pro	Gln
1725					20					25					30		
1726		_		_	_				_	_		_					
1727		Gly	Tyr	Ala	Gly	Pro	Arg	Cys	Glu	Ile	Asp	Val	Asn	Glu	Cys	Leu	Ser
				35					40					45			
1728				33													
1728 1729																	
1728 1729 1730		Asn	Pro		Gln	Asn	Asp		Thr	Cys	Leu	Asp		Ile	Gly	Glu	Phe
1728 1729 1730 1731		Asn	Pro 50		Gln	Asn	Asp	Ser 55	Thr	Cys	Leu	Asp	Gln 60	Ile	Gly	Glu	Phe
1728 1729 1730 1731 1732			50	Cys			_	55		_			60			Glu	Phe
1728 1729 1730 1731 1732 1733		Gln		Cys			Pro	55		_		Leu	60			Glu	Phe
1728 1729 1730 1731 1732			50	Cys				55		_			60			Glu	Phe

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1735 1736																	
1737 1738	(2)	INFO	RMAT:	ION :	FOR :	SEQ :	ID N	0:16	:								
1739 1740 1741 1742 1743		(i)	SEQUAL (A) (B) (C) (D)	) LEI ) TYI ) STI	NGTH PE: 8 RANDI	: 654 amino EDNE:	TERIS 4 am: 5 ac: SS: s unkno	ino a id sing:	acids	3							
1744 1745		/ \															
1746		(ii)	MOLI	2011	<u>.</u>	rc: ]	Jept.	iue									
1747 1748																	
1749																	
1750 1751		(xi)	SEQ	JENC	E DE	SCRI	PTIO	V: SI	EQ II	ои с	:16:						
1751		Thr	Pro	Pro	Gln	Gly	Glu	Ile	Glu	Ala	Asp	Cvs	Met	asp	Val	Asn	Val
1753		1				5					10	•		-		15	
1754		<b>-</b>	~1			<b>~</b> 1	<b>5</b> 1	m1	_	_		~ 7		_	_	_	~7
1755 1756		Arg	GLY	Pro	Asp 20	GIY	Pne	Thr	Pro	Leu 25	Met	тте	Ala	ser	Cys 30	ser	Gly
1757					20					23					30		
1758		Gly	Gly	Leu	Glu	Thr	Gly	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Ser	Ala
1759				35					40					45			
1760 1761		7 00	Mot	т1.	Com	7 an	Dho	т1.	<b>~1</b>	~1 n	~1	777	~1 <del>~</del>	T 011	TT-1 -	7. ~~	(1) m
1761		ASII	Met 50	TIE	361	Asp	PHE	55	GIY	GIII	GIY	Ата	60	цец	птв	ASII	GIII
1763																	
1764			Asp	Arg	Thr	Gly	Glu	Thr	Ala	Leu	His	Leu	Ala	Ala	Arg	Tyr	Ala
1765		65					70					75					80
1766 1767		Ara	Ala	Asp	Ala	Ala	Lvs	Ara	Leu	Leu	Glu	Ser	Ser	Δla	Asp	Ala	Asn
1768		5				85	-1-	3	204		90				····	95	
1769		_	_				_							_		_	
1770		Val	Gln	Asp		Met	Gly	Arg	Thr		Leu	His	Ala	Ala		Ala	Ala
1771 1772					100					105					110		
1773		Asp	Ala	Gln	Gly	Val	Phe	Gln	Ile	Leu	Ile	Arg	Asn	Arg	Ala	Thr	Asp
1774				115					120					125			
1775		Т олл	7 ~~	ח ז ה	7 ~~~	Mot	Dho	7 ~~	<b>a</b> 1	mb as	mh sa	Dwo	T 0	T1.	T	70.7	77-
1776 1777		Leu	130	ALA	Arg	мес	Pne	135	GTĀ	IIII	1111	PIO	140	TTE	Leu	Ата	Ala
1778																	
1779		Arg	Leu	Ala	Val	Glu	Gly	Met	Val	Glu	Glu	Leu	Ile	Asn	Ala	His	Ala
1780		145					150					155					160
1781 1782		Agn	Val	Δen	Δla	Va l	Δen	Glu	Dhe	Glv	Lve	Ser	בומ	T.e.11	Hic	Trn	Δla
1783		wab	Val	H211	AIG	165	Lop	CIU	FIIG	GIY	170	DCI	лıа	Leu	1113	175	ATA
1784																	
1785		Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Ala	Val	Leu	Leu	Lys	Asn	Ser

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1786				180					185					190		
1787 1788	Ala	Asn	Lvs	Asp	Met	Gln	Asn	Asn	Lvs	Glu	Glu	Thr	Ser	Leu	Phe	Leu
1789			195					200	-1-				205			
1790																
1791	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala	Lys	Val	Leu	Leu	Asp	His
1792		210					215					220				
1793																
1794	_	Ala	Asn	Arg	Asp		Thr	Asp	His	Met	Asp	Arg	Leu	Pro	Arg	Asp
1795	225					230					235					240
1796	_	_	_	_						_	_					_
1797	Ile	Ala	Gln	Glu	_	Met	His	His	Asp		Val	His	Leu	Leu	_	Glu
1798					245					250					255	
1799	_	_	_		_	_	_	1	_	'	_	~-7	_	_	~-7	
1800	Tyr	Asn	Leu		гàг	ser	Pro	Thr		His	Asn	GLY	Pro		GIY	Ala
1801				260					265					270		
1802	mb	mb	T	0	Dece	Dana	т1.	<b>G</b>	O	D	7	<b>a</b> 1	m	1.0° - 1-	<b>~1</b>	7
1803 1804	THE	THE	275	ser	Pro	Pro	тте		ser	Pro	ASII	GIY	Tyr	мес	GIY	ASII
1805			2/5					280					285			
1805	Mot	Laze	Dro	Car	V21	Gln	Sar	Larg	Laze	λla	Δνα	T.320	Pro	Sar	т1Д	Lare
1807	1100	290	110	DCI	Val	0111	295	цуз	цуз	AIG	AL 9	300	110	DCI	110	цуз
1808		200					2,7,5					500				
1809	Glv	Asn	Glv	Cvs	Lvs	Glu	Ala	Lvs	Glu	Leu	Lvs	Ala	Arg	Ara	Lvs	Lvs
1810	305		<b>U</b> -1	O <sub>I</sub> D	-1-	310		-1-			315		9	3		320
1811																
1812	Ser	Gln	Asp	Glv	Lvs	Thr	Thr	Leu	Leu	Asp	Ser	Glv	Ser	Ser	Glv	Val
1813			~	•	325					330		-			335	
1814																
1815	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Thr	His	Gly	Tyr	Leu	Ser	Asp
1816				340					345					350		
1817																
1818	Val	Ser	Ser	Pro	Pro	Leu	Met	Thr	Ser	Pro	Phe	Gln	Gln	Ser	Pro	Ser
1819			355					360					365			
1820																
1821	Met		Leu	Asn	His	Leu		Ser	Met	Pro	Glu		Gln	Leu	Gly	Met
1822		370					375					380				
1823	7	TT-2	<b>-</b> 1 -	7	34-4	77 -	ml	T	<b>~1.</b> -	<b>~1</b>	3.6 - L	<b>71</b> -	7 T _	<b>~1</b>	<b>a</b>	n
1824		Hls	тте	Asn	мет		Thr	гуѕ	GIN	GIU		Ата	Ala	GIY	ser	
1825	385					390					395					400
1826 1827	7.~~	Mot	777	Dho	7 00	- ד ת	Mot	1701	Dxo	7 ~~	T 011	The	uia	T 011	7 02	7 T -
1828	Arg	Mec	Ата	Pile	405	Ата	Met	vaı	PIO	410	Leu	1111	His	Leu	415	AIA
1829					403					410					413	
1830	Ser	Ser	Pro	Asn	Thr	Ile	Met	Ser	Asn	Glv	Ser	Met	His	Phe	Thr	Val
1831	001	001	110	420				001	425	017	501		*****	430		Val
1832																
1833	Gly	Gly	Ala	Pro	Thr	Met	Asn	Ser	Gln	Cys	Asp	Trp	Leu	Ala	Arq	Leu
1834	•	-	435					440		4	-	-	445		_	
1835																
1836	Gln	Asn	Gly	Met	Val	Gln	Asn	Gln	Tyr	Asp	Pro	Ile	Arg	Asn	Gly	Ile

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1837			450					455					460				
1838		<b>01</b>	<b>~1</b>	<b>~</b> 1	*	n 7 -	<b>~</b> 1	<b>~</b> 1		<b>~</b> 3	~ 7 -	<b>.</b>	~1	'	~1	_	
1839			GIN	GIY	Asn	Ата		GIN	Ата	GIN	Ата		GIn	His	GIĀ	Leu	
1840		465					470					475					480
1841		m)	<b>a</b>	•	TT 2	<b>3</b>	~1		_		m)	m)	_	_	~ 7		
1842		Thr	ser	Leu	HIS		GIY	ьeu	Pro	Ата		Thr	ьeu	ser	GIN	Met	Met
1843						485					490					495	
1844		m1	m	~1	<b>7.1</b> -	<b>N</b>	D	7	m1	3	<b>T</b>	77.	<b>3</b>	<b>~</b> 1	Б	TT !	•
1845		Thr	Tyr	GIN		Met	Pro	ASI	Thr		ьeu	Ата	Asn	GIN		His	Leu
1846					500					505					510		
1847		N# - +-	<b>~</b> 1	<b>77</b> -	~1	<b>~</b> 1	1.0 m dm	<b>~1</b>	<b>~</b> 13	<b>~</b> 1	<b>a</b> 1	7	<b>.</b>	<b>~1</b>	<b>.</b>		a1
1848		мес	GIN		GIN	GIN	мет	GIN		GIN	GIN	Asn	ьeu		ьeu	His	GIN
1849				515					520					525			
1850		0	3.6 a. da	a1	a1	<b>01</b> -	77.	774 -	*	Q	0	m1	m)	0	m1	773 -	<b>-</b> 1 -
1851		ser		GIN	GIN	GIII	HIS		ASII	ser	ser	Thr		ser	Thr	His	тте
1852			530					535					540				
1853		7	C	Dage	Dha	G	0	C	7	<b>-</b> 1 -	0	<b>~1</b>	ml	7	T	<b>~1</b>	<b>~1</b>
1854 1855			ser	Pro	Pne	Cys		ser	Asp	тте	ser		Thr	Asp	ьeu	Gln	
1856		545					550					555					560
1857		Mot	Sor	Sor	7 cn	λan	Tla	шia	602	17-1	Mot	Dro	Cln	7 an	Thr	Cln	Tlo
1858		Mec	Set	SET	ASII	565	116	птэ	per	vaı	570	PIO	GIII	Asp	1111	Gln 575	TTE
1859	•					505					370					3/3	
1860		Phe	Δla	Δla	Ser	T.e11	Pro	Ser	Δgn	T.e.11	Thr	Gln	Ser	Met	Thr	Thr	Δla
1861		1110	niu	mu	580	Leu	110	DCI	71011	585	1111	Q111	DCI	HCC	590	T 11T	ALG
1862					500					505					330		
1863		Gln	Phe	Leu	Thr	Pro	Pro	Ser	Gln	His	Ser	Tvr	Ser	Ser	Pro	Met	Asp
1864		02		595					600			- 1 -		605			
1865									•••								
1866		Asn	Thr	Pro	Ser	His	Gln	Leu	Gln	Val	Pro	Asp	His	Pro	Phe	Leu	Thr
1867			610					615					620				
1868																	
1869		Pro	Ser	Pro	Glu	Ser	Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser
1870		625					630	-		-		635					640
1871																	
1872		Asn	Met	Ser	Asp	Trp	Ser	Glu	Gly	Ile	Ser	Ser	Pro	Pro	Thr		
1873					_	645			_		650						
1874																	
1875	(2)	INFO	RMAT	I NO	FOR S	SEQ :	D NO	0:17	:								
1876															•		
1877		(i)	SEQU	JENCI	E CH	ARAC	CERIS	STICS	3:								
1878						: 666			acids	3							
1879						amino											
1880						EDNES			le								
1881			(D)	TO	OLO	3Υ: ι	ınkno	own									
1882																	
1883		(ii)	MOLI	ECULI	TYI	PE: I	pept	ıde									
1884																	
1885																	
1886		(3x ÷ )	CEC	יייאנאיי	יים בו	CDT	ייי דייייני	T. CT	70 TT	) NTA	. 1 77 .						
1887		(xi)	2EQ(	) ENC!	י אים	OCKI	TIOE	N: 21	דד אי	י אט י	Ι						

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1000																
1888 1889	The	Dro	Dro	C1 2	C1	C1.,	1701	7.00	71-	7. ~~	Crea	Mot	7	1707	7 ~~	1707
1890	1	PIO	PIO	GIII	5 5	GIU	vaı	ASP	мта	10	Суѕ	Mec	Asp	vaı	Asn 15	vaı
1891	т				5					10					13	
1892	7 20	C111	Dro	7) cm	C111	Dho	Thr	Dro	T 011	Mot	T1.	ת ז ת	802	Crra	Ser	C1.,
1893	Arg	Gry	PIO	20	GIY	FIIE	1111	PIO		Met	116	ніа	ser		Ser	GIY
1894				20					25					30		
1895	Clar	C117	T 011	Clu	Thr	C1.	7 an	602	C1,,	C1.,	C1,,	C1.,	7 an	77.	Pro	71-
1896	GIY	СТУ	35	GIU	1111	СТУ	ASII	40	GIU	GIU	GIU	Gru	45	ALA	PIO	Ala
			33					40					45			
1897 1898	1707	т	Com	7 ~~	Dho	т1.	TT= ===	۵1 m	a1	71.	C 0 20	T 0	TT	7	<b>~1</b>	mla sa
	vaı		ser	Asp	Pne	тте	_	GIII	Gry	AIa	Ser	60	птъ	ASII	Gln	TIII
1899 1900		50					55					60				
1901	7 an	7 200	Thr	G1.	C1.,	Thr	71-	T 011	ui a	T 011	ת ד ת	717	7. ~~~	Tres	Ser	7. ~~
1902	65	Arg	1111	Gry	GIU	70	нта	ьеu	птр	ьeu	75	ALA	Arg	ıyı	ser	_
1902	65					70					/5					80
1904	802	7 an	ת 1 ת	717	Tara	7/200	T 011	T 011	C1.,	717	602	ת 1 ת	7 an	7.1.	Asn	T10
1905	Ser	ASP	нта	Ата	БуS 85	Arg	пеп	ьeu	GIU	90	ser	нта	ASP	нта		116
1906					65					90					95	
1907	Gln	λen	λan	Mot	Gl v	λνα	Thr	Dro	T.611	uic	בות	λla	Wa I	Car	Ala	7 cm
1908	GLII	чэр	Wali	100	GIY	Arg	1111	FIU	105	шъ	Ата	AIa	val	110	AIA	Asp
1909				100					105					110		
1910	Δla	Gln	Glv	Va 1	Dhe	Gln	Tla	T.011	T.011	λrα	λan	λrα	λΊэ	Thr	Asp	T.011
1911	Ала	GIII	115	vai	FIIC	GIII	116	120	Бец	Arg	Poli	Arg	125	1111	ASP	пеи
1912			113					120					123			
1913	Δen	Δla	Δra	Met	Hie	Asn	Glv	Thr	Thr	Pro	T.e.11	Tle	T.e.11	Δla	Ala	Δrα
1914	пор	130	y	1100	*****	nop	135	1111	1111	110	LCu	140	Lea	niu	ALG	nr 9
1915																
1916	T.em	Δla	Val	Glu	Glv	Met	T.e11	Glu	Δsn	T.e11	Tle	Δsn	Ser	His	Ala	Asn
1917	145		• • • •	· ·	O <sub>T</sub>	150			· · · · ·	200	155		001			160
1918																
1919	Val	Asn	Ala	Val	Asp	Asp	Leu	Glv	Lvs	Ser	Ala	Leu	His	Trp	Ala	Ala
1920					165	F		1	-1-	170					175	
1921																
1922	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val	Val	Leu	Leu	Lvs	Asn	Gly	Ala
1923				180		-			185				-	190	-	
1924																
1925	Asn	Lys	Asp	Met	Gln	Asn	Asn	Lys	Glu	Glu	Thr	Pro	Leu	Phe	Leu	Ala
1926		_	195					200					205			
1927																
1928	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala	Lys	Val	Leu	Leu	Asp	His	Phe
1929		210		_		-	215			_		220		_		
1930																
1931	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg	Leu	Pro	Arg	Asp	Ile
1932	225		_	_		230	_			_	235				_	240
1933																
1934	Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile	Val	Arg	Leu	Leu	Asp	Glu	Tyr
1935					245					250					255	
1936																
1937	Asn	Leu	Val	Arg	Ser	Pro	Gln	Leu	His	Gly	Thr	Ala	Leu	Gly	Gly	Thr
1938				260					265					270		

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1939																
1940	Pro	Thr	T.011	Sar	Dro	Thr	T.A11	Cve	Sar	Dro	λan	Glv	Tur	T.011	Glaz	Asn
1941	110	1111	275	DCI	110	1111	шси	280	DCI	110	71011	O.L.y	285	LCu	O <sub>T</sub> y	Abii
1942			2,5					200					203			
1943	T.611	Tare	Sar	Δla	Thr	Gln	Glaz	Larg	Tage	Δla	Ara	Laze	Dro	Ser	Thr	Larg
1944	шса	290	501	niu		0111	295	шуо	шур	7114	9	300		501		-75
1945		2,70					2))					500				
1946	G] v	T.611	7 l s	Cve	Sar	Ser	Lvc	Glu	Δla	Tare	Δan	T.e.11	Larg	Ala	Δrα	Δrα
1947	305	пец	Ата	Cys	261	310	цуз	Gru	Ата	цуз	315	пец	цуз	AIA	Arg	320
1948	303					210					313					320
1949	Tara	T 110	Cox	Cln	7 an	C1.,	Tara	C3.11	Crra	T 011	T 011	7 00	Cor	Ser	802	Mot
1950	цуѕ	цуѕ	Ser	GIII	325	GIY	цуъ	GIY	Cys	330	пец	App	PCT	Ser	335	Mec
1951					323					330					333	
1952	T 011	Sor	Dro	77-1	Λαn	Car	Len	Glu	Car	Dro	Uic	Glaz	Тиг	Leu	Sar	λen
1953	пеп	Ser	PIO	340	Asp	261	пеп	GIU	345	PIO	птэ	Gry	тут	350	Ser	Asp
1954				340					343					330		
1954	1707	77.	C0.x	Dro	Dro	T 011	Dro	Cor	Dro	Dho	Cln	Cln.	cor	Pro	Cor	Mot
1956	Val	Ala	355	PLO	PIO	ьeu	PIO	360	PIO	Pile	GIII	GIII	365	PIO	Ser	MEC
1957			333					300					303			
1957	Dro	T 011	802	uic	T 011	Dro	C111	Mot	Dro	λan	Thr	шic	LOU	Gly	т1о	Sor
1959	PIO	370	ser	птэ	пеп	PIO	375	Mec	PIO	ASP	1111	380	Leu	GIY	TIE	Ser
1960		3/0					3/3					300				
1961	uic	T 011	7 an	1701	ת בות	ת ד ת	T 320	Dro	C111	Mot	Nlα	ת 1 ת	T 011	Ala	Glv	Clv
1962		Leu	ASII	vaı	АТА	390	цур	PIO	GIU	Mec	395	Ата	пец	Ата	GLY	400
	385					390					333					400
1963	C - 22	7 24~	T 011	77.	Dho	<b>~1.</b> ,	Dro	Dwo	Dro	Dro	7. ~~	T 011	602	uic	T 011	Dro
1964	ser	Arg	ьeu	AIA		GIU	PIO	PLO	PIO		Arg	пеп	Ser	His	415	PIO
1965					405					410					413	
1966	7707	77.	C 0.70	Cox	717	Cox	The	1701	T 011	602	Thr	7 an	C111	Thr	C137	ת דת
1967	vaı	ALA	ser		Ата	ser	1111	vai	425	ser	1111	ASII	СТУ	430	GIY	Ата
1968 1969				420					423					430		
1970	Mot	7 an	Dho	Thr	1727	Clv	717	Dro	712	Car	Len	λan	Glv	Gln	Care	Glu
1970	Mec	ASII	435	1111	vaı	GIY	на	440	Ата	SET	пеи	MOII	445	GIII	Cys	Giu
1972			433					110					117			
1972	Trn	T.011	Dro	λνα	T.011	Gln	λen	Glv	Mot	Va l	Dro	Sar	Gln	Tyr	Δen	Dro
1974	115	450	FIO	Arg	пси	0111	455	OLY	I-IC C	Val	110	460	0111	- 7 -	71011	110
1975		430					433					100				
1976	T.e.11	Δrσ	Pro	Glv	Val	Thr	Pro	Glv	Thr	Len	Ser	Thr	Gln	Ala	Δla	Glv
1977	465	m 9	110	CLY	V 04.1	470	110	017			475		<b>01</b>			480
1978	403					1,0					1,5					100
1979	Leu	Gln	His	Glv	Met	Met	Ser	Pro	Tle	His	Ser	Ser	Leu	Ser	Thr	Asn
1980		01	*****	017	485					490					495	
1981																
1982	Thr	Leu	Ser	Pro	Ile	Ile	Tvr	Gln	Glv	Leu	Pro	Asn	Thr	Arg	Leu	Ala
1983			~~~	500			- 1		505					510		
1984																
1985	Thr	Gln	Pro	His	Leu	Val	Gln	Thr	Gln	Gln	Val	Gln	Pro	Gln	Asn	Leu
1986			515					520		_	_	_	525			
1987								-								
1988	Gln	Ile	Gln	Pro	Gln	Asn	Leu	Gln	Pro	Pro	Ser	Gln	Pro	His	Leu	Ser
1989		530	_		_		535					540				

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1990 1991 1992 1945 19545 1955 19560 1955 19560 1957 1958 1958 1958 1958 1959 1959 1959 1959
1992   545   550   555   560   1993   1994   1995   565   565   565   565   565   570   570   575   575   1995   565   565   565   570   570   575   575   1996   1997   Val His Thr Ile Leu Pro Gln Glu Ser Gln Ala Leu Pro Thr Ser Leu Pro 1998   580   580   585   585   590   590   590   590   590   590   590   590   605
1993 1994 1994 1995 1995 1996 1997 1996 1997 1998 1997 1998 1999 1999 1999 1999
1994   Glu Pro Ser Gln Ala Asp Val Gln Pro Leu Gly Pro Ser Ser Leu Pro 1995   1996   1997   1996   1997   1998   1999
1995   565   570   575   575   1996   1997   1997   1998   580   580   580   585   580   585   580   580   580   580   585   580   580   590   1999
1996 1997 1998 1998 1999 2000 1998 2000 1998 2000 1998 2000 2001 1998 2000 2001 2002 2002 2003 2004 2006 2006 2007 2007 2008 2008 2008 2008 2009 2009 2000 2009 2000 2001 2002 2001 2002 2003 2004 2005 2006 2006 2006 2007 2007 2008 2008 2009 2008 2009 2009 2009 2009
1997
1998
1999 2000
Pro   Ser   Ser   Met   Val   Pro   Pro   Met   Thr   Thr   Thr   Gln   Phe   Leu   Thr   Pro   2001   595   595   595   600   600   605
2001
2002 2003 2004 2004 2004 2005 2006 2006 2007 2007 2007 2008 2009 2009 2009 2009 2009 2001 2011 2012 2013 2014 2015 2014 2015 2016 2017 2017 2018 2018 2019 2019 2019 2010 2010 2010 2011 2011
Pro   Ser   Gln   His   Ser   Tyr   Ser   Ser   Pro   Val   Asp   Asn   Thr   Pro   Ser   2004   610   615   615   615   620   620   620   620   620   620   620   620   620   620   620   625   630   630   630   635   635   630   640   640   620   625   625   630   630   630   635   635   635   655   655   655   655   655   620   620   625   625   630   645   625   625   625   620   645   625
2004 610 615 620 2006 His Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr Pro Ser Pro Glu 2007 625 630 630 635 640 2008 2009 Ser Pro Asp Gln Trp Ser Ser Ser Ser Arg His Ser Asn Ile Ser Asp 2010 645 655 650 655 2011 2012 Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr 2013 660 665 2014 2015 (2) INFORMATION FOR SEQ ID NO:18: 2016 2017 (i) SEQUENCE CHARACTERISTICS: 2018 (A) LENGTH: 681 amino acids 2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2006 2006 2007 2007 2007 2007 2008 2008 2009 2009 2009 2007 2007 2008 2009 2008 2009 2009 2008 2009 2009
2006
2007 625 630 635 640 2008 2009 Ser Pro Asp Gln Trp Ser Ser Ser Arg His Ser Asn Ile Ser Asp 2010 645 655 650 655 2011 2012 Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr 660 665 2014 2015 (2) INFORMATION FOR SEQ ID NO:18: 2016 (i) SEQUENCE CHARACTERISTICS: 2018 (A) LENGTH: 681 amino acids 2019 (C) STRANDEDNESS: single 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034 2034
2008 2009
Ser Pro Asp Gln Trp Ser Ser Ser Ser Arg His Ser Asn Ile Ser Asp 2010
2010 645 650 655 2011 2012 Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr 2013 660 665 2014 2015 (2) INFORMATION FOR SEQ ID NO:18: 2016 2017 (i) SEQUENCE CHARACTERISTICS: 2018 (A) LENGTH: 681 amino acids 2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2034
2011 2012     Trp Ser Glu Gly Ile Ser Ser Pro Pro Thr 2013     660    665  2014 2015 2016 2017 (i) SEQUENCE CHARACTERISTICS: 2018     (A) LENGTH: 681 amino acids 2019     (B) TYPE: amino acid 2020     (C) STRANDEDNESS: single 2021     (D) TOPOLOGY: unknown 2022 2023 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029     Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030     1     5     10    15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2012
2013 660 665 2014 2015 (2) INFORMATION FOR SEQ ID NO:18: 2016 2017 (i) SEQUENCE CHARACTERISTICS: 2018 (A) LENGTH: 681 amino acids 2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2014 2015 (2) INFORMATION FOR SEQ ID NO:18: 2016 2017 (i) SEQUENCE CHARACTERISTICS: 2018 (A) LENGTH: 681 amino acids 2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2015 (2) INFORMATION FOR SEQ ID NO:18: 2016 2017 (i) SEQUENCE CHARACTERISTICS: 2018 (A) LENGTH: 681 amino acids 2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2016 2017 (i) SEQUENCE CHARACTERISTICS: 2018 (A) LENGTH: 681 amino acids 2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2017 (i) SEQUENCE CHARACTERISTICS: 2018 (A) LENGTH: 681 amino acids 2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2018 (A) LENGTH: 681 amino acids 2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2019 (B) TYPE: amino acid 2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2020 (C) STRANDEDNESS: single 2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2021 (D) TOPOLOGY: unknown 2022 2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2022 2023
2023 (ii) MOLECULE TYPE: peptide 2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2024 2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2025 2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2026 2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18: 2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2027 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  2028  2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15  2031  2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2028 2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2029 Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val 2030 1 5 10 15 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2030 1 5 10 15 2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 2034
2031 2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 20 25 30 2034
2032 Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 2033 20 25 30 2034
2033 20 25 30 2034
2034
2035 Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Pro Ala
2036 35 40 45
2037
2038 Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr
2039 50 55 60 2040

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DATE: 12/16/93 TIME: 13:12:01

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2044 2045 2046	Ser	Asp	Ala	Ala	Lys 85	Arg	Leu	Leu	Glu	Ala 90	Ser	Ala	Asp	Ala	Asn 95	Ile
2047 2048 2049	Gln	Asp	Asn	Met 100	Gly	Arg	Thr	Pro	Leu 105	His	Ala	Ala	Val	Ser 110	Ala	Asp
2050 2051 2052	Ala	Gln	Gly 115	Val	Phe	Gln	Ile	Leu 120	Ile	Arg	Asn	Arg	Ala 125	Thr	Asp	Leu
2053 2054 2055	Asp	Ala 130	Arg	Met	His	Asp	Gly 135	Thr	Thr	Pro	Leu	Ile 140	Leu	Ala	Ala	Arg
2056 2057 2058	Leu 145	Ala	Val	Glu	Gly	Met 150	Leu	Glu	Asp	Leu	Ile 155	Asn	Ser	His	Ala	Asp 160
2059 2060 2061					165			_	_	170				_	Ala 175	
2062 2063 2064	Ala	Val	Asn	Asn 180	Val	Asp	Ala	Ala	Val 185	Val	Leu	Leu	Lys	Asn 190	Gly	Ala
2065 2066 2067	Asn	Lys	Asp 195	Met	Gln	Asn	Asn	Arg 200	Glu	Glu	Thr	Pro	Leu 205	Phe	Leu	Ala
2068 2069 2070		210		_			215			_		220		_	His	
2071 2072 2073	225			_		230	_			_	235			_	Asp	240
2074 2075 2076					245			_		250				-	Glu 255	-
2077 2078 2079				260					265					270	Gly	
2080 2081 2082			275					280					285		Gly	
2083 2084 2085	Leu	Lys 290	Pro	Gly	Val	Gln	Gly 295	Lys	Lys	Val	Arg	300	Pro	Ser	Ser	Lys
2086 2087 2088	305					310					315				Arg	320
2089 2090 2091	Lys	Lys	Ser	Gln	Asp 325	Gly	Lys	Gly	Cys	Leu 330	Leu	Asp	Ser	Ser	Gly 335	Met

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

INPUT SET: S7068.raw

DATE: 12/16/93 TIME: 13:12:08

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2095 2096 2097	Val	Ala	Ser 355	Pro	Pro	Leu	Leu	Pro 360	Ser	Pro	Phe	Gln	Gln 365	Ser	Pro	Ser
2098 2099 2100	Val	Pro 370	Leu	Asn	His	Leu	Pro 375	Gly	Met	Pro	Asp	Thr 380	His	Leu	Gly	Ile
2101 2102 2103	Gly 385	His	Leu	Asn	Val	Ala 390	Ala	Lys	Pro	Glu	Met 395	Ala	Ala	Leu	Gly	Gly 400
2104 2105 2106	Gly	Gly	Arg	Leu	Ala 405	Phe	Glu	Thr	Gly	Pro 410	Pro	Arg	Leu	Ser	His 415	Leu
2107 2108 2109	Pro	Val	Ala	Ser 420	Gly	Thr	Ser	Thr	Val 425	Leu	Gly	Ser	Ser	Ser 430	Gly	Gly
2110 2111 2112	Ala	Leu	Asn 435	Phe	Thr	Val	Gly	Gly 440	Ser	Thr	Ser	Leu	Asn 445	Gly	Gln	Cys
2113 2114 2115	Glu	Trp 450	Leu	Ser	Arg	Leu	Gln 455	Ser	Gly	Met	Val	Pro 460	Asn	Gln	Tyr	Asn
2116 2117 2118	Pro 465	Leu	Arg	Gly	Ser	Val 470	Ala	Pro	Gly	Pro	Leu 475	Ser	Thr	Gln	Ala	Pro 480
2119 2120 2121	Ser	Leu	Gln	His	Gly 485	Met	Val	Gly	Pro	Leu 490	His	Ser	Ser	Leu	Ala 495	Ala
2122 2123 2124	Ser	Ala	Leu	Ser 500	Gln	Met	Met	Ser	Tyr 505	Gln	Gly	Leu	Pro	Ser 510	Thr	Arg
2125 2126 2127	Leu	Ala	Thr 515	Gln	Pro	His	Leu	Val 520	Gln	Thr	Gln	Gln	Val 525	Gln	Pro	Gln
2128 2129 2130	Asn	Leu 530	Gln	Met	Gln	Gln	Gln 535	Asn	Leu	Gln	Pro	Ala 540	Asn	Ile	Gln	Gln
2131 2132 2133	Gln 545		Ser	Leu		Pro 550		Pro	Pro	Pro	Pro 555		Pro	His	Leu	Gly 560
2134 2135 2136	Val	Ser	Ser	Ala	Ala 565	Ser	Gly	His	Leu	Gly 570	Arg	Ser	Phe	Leu	Ser 575	Gly
2137 2138 2139	Glu	Pro	Ser	Gln 580	Ala	Asp	Val	Gln	Pro 585	Leu	Gly	Pro	Ser	Ser 590	Leu	Ala
2140 2141 2142	Val	His	Thr 595	Ile	Leu	Pro	Gln	Glu 600	Ser	Pro	Ala	Leu	Pro 605	Thr	Ser	Leu

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DATE: 12/16/93 TIME: 13:12:15

2143 2144		Pro	Ser 610	Ser	Leu	Val	Pro	Pro 615	Val	Thr	Ala	Ala	Gln 620	Phe	Leu	Thr	Pro
2145		<b>D</b>	<b>a</b>	<b>~</b> 1 .	'	_		_	_	_		~-	_	1	_	_	
2146			ser	GIN	HIS	ser	_	ser	ser	Pro	Val		Asn	Thr	Pro	Ser	
2147 2148		625					630					635					640
2149		Gln	T.011	Gln	Va 1	Pro	Glu	Hic	Dro	Dhe	T.A11	Thr	Dro	Car	Dro	Glu	Sar
2150		GIII	пец	GIII	vai	645	GIU	птэ	PIO	FIIC	650	1111	PIO	SET	PIO	655	Ser
2151						015					030					033	
2152		Pro	Asp	Gln	Trp	Ser	Ser	Ser	Ser	Pro	His	Ser	Asn	Val	Ser	Asp	Trp
2153				-	660					665					670	F	<b>F</b>
2154																	
2155		Ser	Glu	Gly	Val	Ser	Ser	Pro	Pro	Thr							
2156				675					680								
2157																	
2158	(2)	INFO	RMAT:	ON I	FOR S	SEQ :	ID NO	0:19	:								
2159																	
2160		(i)	SEQU	JENCI	E CHA	ARAC:	TERIS	STICS	S:								
2161					NGTH				acio	ls							
2162					PE: 8												
2163					RANDI			_	le								
2164			(D)	TO	POLO	3Υ: ι	ınkno	own									
2165		,						. ,									
2166		(ii)	MOLI	COL	E TYI	?E: I	pept:	ıde									
2167																	
2168																	
2169		( <b>v</b> i)	g E O I	TENICI	ישת ב	CDTI	ירדר	J. CI	70 TI	) NO	.10.						
2169 2170		(xi)	SEQU	JENCI	E DES	SCRII	PTIO	1: SI	EQ II	ONO	:19:						
2169 2170 2171												Δla	I.e.i	I.eu	Δla	T.e.u	Trn
2169 2170 2171 2172		Met				Arg					Trp	Ala	Leu	Leu	Ala	Leu 15	Trp
2169 2170 2171 2172 2173												Ala	Leu	Leu	Ala	Leu 15	Trp
2169 2170 2171 2172		Met 1	Pro	Ala	Leu	Arg 5	Pro	Ala	Leu	Leu	Trp 10					15	_
2169 2170 2171 2172 2173 2174		Met 1	Pro	Ala	Leu	Arg 5	Pro	Ala	Leu	Leu	Trp 10						_
2169 2170 2171 2172 2173 2174 2175		Met 1	Pro	Ala	Leu Ala	Arg 5	Pro	Ala	Leu	Leu Ala	Trp 10				Asp	15	_
2169 2170 2171 2172 2173 2174 2175 2176		Met 1 Leu	Pro Cys	Ala Cys	Leu Ala 20	Arg 5 Ala	Pro Pro	Ala Ala	Leu His	Leu Ala 25	Trp 10 Leu	Gln	Cys	Arg	Asp 30	15	Туг
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179		Met 1 Leu	Pro Cys	Ala Cys	Leu Ala 20	Arg 5 Ala	Pro Pro	Ala Ala	Leu His	Leu Ala 25	Trp 10 Leu	Gln	Cys	Arg	Asp 30	15 Gly	Туг
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180		Met 1 Leu Glu	Pro Cys Pro	Ala Cys Cys 35	Leu Ala 20 Val	Arg 5 Ala Asn	Pro Pro Glu	Ala Ala Gly	Leu His Met	Leu Ala 25 Cys	Trp 10 Leu Val	Gln Thr	Cys Tyr	Arg His 45	Asp 30 Asn	15 Gly Gly	Tyr Thr
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181		Met 1 Leu Glu	Pro Cys Pro Tyr	Ala Cys Cys 35	Leu Ala 20 Val	Arg 5 Ala Asn	Pro Pro Glu	Ala Ala Gly Glu	Leu His Met	Leu Ala 25 Cys	Trp 10 Leu Val	Gln Thr	Cys Tyr	Arg His 45	Asp 30 Asn	15 Gly	Tyr Thr
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182		Met 1 Leu Glu	Pro Cys Pro	Ala Cys Cys 35	Leu Ala 20 Val	Arg 5 Ala Asn	Pro Pro Glu	Ala Ala Gly	Leu His Met	Leu Ala 25 Cys	Trp 10 Leu Val	Gln Thr	Cys Tyr	Arg His 45	Asp 30 Asn	15 Gly Gly	Tyr Thr
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183		Met 1 Leu Glu Gly	Pro Cys Pro Tyr 50	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys	Arg 5 Ala Asn Cys	Pro Pro Glu Pro	Ala Ala Gly Glu 55	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu	Gln Thr Gly	Cys Tyr Glu 60	Arg His 45 Tyr	Asp 30 Asn Cys	Gly Gly Gln	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184		Met 1 Leu Glu Gly	Pro Cys Pro Tyr 50	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys	Arg 5 Ala Asn Cys	Pro Pro Glu Pro Lys	Ala Ala Gly Glu 55	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu	Gln Thr Gly Asn	Cys Tyr Glu 60	Arg His 45 Tyr	Asp 30 Asn Cys	15 Gly Gly	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185		Met 1 Leu Glu Gly	Pro Cys Pro Tyr 50	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys	Arg 5 Ala Asn Cys	Pro Pro Glu Pro	Ala Ala Gly Glu 55	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu	Gln Thr Gly	Cys Tyr Glu 60	Arg His 45 Tyr	Asp 30 Asn Cys	Gly Gly Gln	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186		Met 1 Leu Glu Gly Arg 65	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys Cys	Arg 5 Ala Asn Cys Glu	Pro Glu Pro Lys 70	Ala Gly Glu 55 Asn	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu Gln	Gln Thr Gly Asn 75	Cys Tyr Glu 60 Gly	Arg His 45 Tyr	Asp 30 Asn Cys	Gly Gly Gln Cys	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187		Met 1 Leu Glu Gly Arg 65	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys Cys	Arg 5 Ala Asn Cys Glu Leu	Pro Glu Pro Lys 70	Ala Gly Glu 55 Asn	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu Gln	Gln Thr Gly Asn 75	Cys Tyr Glu 60 Gly	Arg His 45 Tyr	Asp 30 Asn Cys	Gly Gln Cys Gly	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188		Met 1 Leu Glu Gly Arg 65	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys	Leu Ala 20 Val Lys Cys	Arg 5 Ala Asn Cys Glu	Pro Glu Pro Lys 70	Ala Gly Glu 55 Asn	Leu His Met 40 Gly	Leu Ala 25 Cys Phe	Trp 10 Leu Val Leu Gln	Gln Thr Gly Asn 75	Cys Tyr Glu 60 Gly	Arg His 45 Tyr	Asp 30 Asn Cys	Gly Gly Gln Cys	Tyr Thr His
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188		Met 1 Leu Glu Gly Arg 65 Ala	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys Pro	Leu Ala 20 Val Lys Cys Met	Arg 5 Ala Asn Cys Glu Leu 85	Pro Glu Pro Lys 70 Gly	Ala Gly Glu 55 Asn Lys	Leu His Met 40 Gly Arg	Leu Ala 25 Cys Phe Cys	Trp 10 Leu Val Leu Gln Cys 90	Gln Thr Gly Asn 75 Arg	Cys Tyr Glu 60 Gly Cys	Arg His 45 Tyr Gly	Asp 30 Asn Cys Thr	Gly Gln Cys Gly 95	Tyr Thr His Val 80 Phe
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190		Met 1 Leu Glu Gly Arg 65 Ala	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys Pro	Leu Ala 20 Val Lys Cys Met Asp	Arg 5 Ala Asn Cys Glu Leu 85	Pro Glu Pro Lys 70 Gly	Ala Gly Glu 55 Asn Lys	Leu His Met 40 Gly Arg	Leu Ala 25 Cys Phe Cys Thr	Trp 10 Leu Val Leu Gln Cys 90	Gln Thr Gly Asn 75 Arg	Cys Tyr Glu 60 Gly Cys	Arg His 45 Tyr Gly	Asp 30 Asn Cys Thr Ser	Gly Gln Cys Gly	Tyr Thr His Val 80 Phe
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188		Met 1 Leu Glu Gly Arg 65 Ala	Pro Cys Pro Tyr 50 Asp	Ala Cys Cys 35 Cys Pro	Leu Ala 20 Val Lys Cys Met	Arg 5 Ala Asn Cys Glu Leu 85	Pro Glu Pro Lys 70 Gly	Ala Gly Glu 55 Asn Lys	Leu His Met 40 Gly Arg	Leu Ala 25 Cys Phe Cys	Trp 10 Leu Val Leu Gln Cys 90	Gln Thr Gly Asn 75 Arg	Cys Tyr Glu 60 Gly Cys	Arg His 45 Tyr Gly	Asp 30 Asn Cys Thr	Gly Gln Cys Gly 95	Tyr Thr His Val 80 Phe
2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191		Met 1 Leu Glu Gly Arg 65 Ala	Pro Cys Pro Tyr 50 Asp Gln Gly	Ala Cys Cys 35 Cys Pro Ala Glu	Leu Ala 20 Val Lys Cys Met Asp 100	Arg 5 Ala Asn Cys Glu Leu 85 Cys	Pro Glu Pro Lys 70 Gly Gln	Ala Gly Glu 55 Asn Lys	Leu His Met 40 Gly Arg Ala	Leu Ala 25 Cys Phe Cys Thr	Trp 10 Leu Val Leu Gln Cys 90 Ser	Gln Thr Gly Asn 75 Arg	Cys Tyr Glu 60 Gly Cys	Arg His 45 Tyr Gly Ala Cys	Asp 30 Asn Cys Thr Ser	Gly Gln Cys Gly 95	Tyr Thr His Val 80 Phe

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DATE: 12/16/93 TIME: 13:12:22

2194			115					120					125			
2195																
2196	Tyr	Glu	Cys	${ t Thr}$	Cys	Gln	Val	Gly	Phe	Thr	Gly	Lys	Glu	Cys	Gln	Trp
2197		130					135					140				
2198																
2199	Thr	Asp	Ala	Cys	Leu	Ser	His	Pro	Cys	Ala	Asn	Gly	Ser	Thr	Cys	Thr
2200	145					150					155					160
2201																
2202	Thr	Val	Ala	Asn	Gln	Phe	Ser	Cys	Lys	Cys	Leu	Thr	Gly	Phe	Thr	Gly
2203					165					170					175	
2204																
2205	Gln	Lys	Cys	Glu	Thr	Asp	Val	Asn	Glu	Cys	Asp	Ile	Pro	Gly	His	Cys
2206				180					185					190		_
2207																
2208	Gln	His	Gly	Gly	Thr	Cys	Leu	Asn	Leu	Pro	Gly	Ser	Tyr	Gln	Cys	Gln
2209			195	_				200			_		205		_	
2210																
2211	Cys	Pro	Gln	Gly	Phe	Thr	Gly	Gln	Tyr	Cys	Asp	Ser	Leu	Tyr	Val	Pro
2212	-	210		_			215		_	_	_	220		-		
2213																
2214	Cys	Ala	Pro	Ser	Pro	Cys	Val	Asn	Gly	Gly	Thr	Cys	Arg	Gln	Thr	Gly
2215	225					230			•	-	235	•	_			240
2216																
2217	Asp	Phe	Thr	Phe	Glu	Cys	Asn	Cys	Leu	Pro	Gly	Phe	Glu	Gly	Ser	Thr
2218	-				245	•		•		250	•			•	255	
2219																
2220	Cys	Glu	Arq	Asn	Ile	Asp	Asp	Cys	Pro	Asn	His	Arq	Cys	Gln	Asn	Gly
2221	•			260		-	_	•	265				-	270		•
2222																
2223	Gly	Val	Cvs	Val	Asp	Gly	Val	Asn	Thr	Tvr	Asn	Cvs	Arq	Cvs	Pro	Pro
2224	1		275			1		280		-1-		-1-	285	-1-		
2225																
2226	Gln	Trp	Thr	Glv	Gln	Phe	Cvs	Thr	Glu	asa	Val	Asp	Glu	Cvs	Leu	Leu
2227		290		•			295			-		300		•		
2228																
2229	Gln	Pro	Asn	Ala	Cys	Gln	Asn	Gly	Gly	Thr	Cys	Ala	Asn	Arq	Asn	Gly
2230	305				•	310		•	•		315			_		320
2231																
2232	Gly	Tyr	Gly	Cys	Val	Cys	Val	Asn	Gly	Trp	Ser	Gly	Asp	Asp	Cys	Ser
2233	-	•	-	-	325	-			•	330		•	•	-	335	
2234																
2235	Glu	Asn	Ile	Asp	Asp	Cys	Ala	Phe	Ala	Ser	Cys	Thr	Pro	Gly	Ser	Thr
2236				340	-	-			345		-			350		
2237																
2238	Cys	Ile	Asp	Arq	Val	Ala	Ser	Phe	Ser	Cys	Met	Cys	Pro	Glu	Gly	Lys
2239	•		355					360		-		-	365		-	-
2240																
2241	Ala	Gly	Leu	Leu	Cys	His	Leu	Asp	Asp	Ala	Cys	Ile	Ser	Asn	Pro	Cys
2242		370			-		375	-	-		-	380				-
2243																
2244	His	Lys	Gly	Ala	Leu	Cys	Asp	Thr	Asn	Pro	Leu	Asn	Gly	Gln	Tyr	Ile

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2245	385					390					395					400
2246						_			_	_						
2247	Cys	Thr	Cys	Pro		Gly	Tyr	Lys	Gly	Ala	Asp	Cys	Thr	Glu	Asp	Val
2248					405					410					415	
2249				_		_										
2250	Asp	Glu	Cys		Met	Ala	Asn	Ser		Pro	Cys	Glu	His	Ala	Gly	Lys
2251				420					425					430		
2252																
2253	Cys	Val	Asn	Thr	Asp	Gly	Ala	Phe	His	Cys	Glu	Cys	Leu	Lys	Gly	${ t Tyr}$
2254			435					440					445			
2255																
2256	Ala	Gly	Pro	Arg	Cys	Glu	Met	Asp	Ile	Asn	Glu	Cys	His	Ser	Asp	Pro
2257		450					455					460				
2258																
2259	Cys	Gln	Asn	Asp	Ala	Thr	Cys	Leu	Asp	Lys	Ile	Gly	Gly	Phe	Thr	Cys
2260	465					470					475					480
2261																
2262	Leu	Cys	Met	Pro	Gly	Phe	Lys	Gly	Val	His	Cys	Glu	Leu	Glu	Ile	Asn
2263					485					490					495	
2264																
2265	Glu	Cys	Gln	Ser	Asn	Pro	Cys	Val	Asn	Asn	Gly	Gln	Cys	Val	Asp	Lys
2266				500					505					510		
2267																
2268	Val	Asn	Arg	Phe	Gln	Cys	Leu	Cys	Pro	Pro	Gly	Phe	Thr	Gly	Pro	Val
2269			515					520					525			
2270																
2271	Cys	Gln	Ile	Asp	Ile	Asp	Asp	Cys	Ser	Ser	Thr	Pro	Cys	Leu	Asn	Gly
2272		530					535					540				
2273																
2274	Ala	Lys	Cys	Ile	Asp	His	Pro	Asn	Gly	Tyr	Glu	Cys	Gln	Cys	Ala	Thr
2275	545					550					555					560
2276																
2277	Gly	Phe	Thr	Gly	Val	Leu	Cys	Glu	Glu	Asn	Ile	Asp	Asn	Cys	Asp	Pro
2278					565					570					575	
2279																
2280	Asp	Pro	Cys	His	His	Gly	Gln	Cys	Gln	Asp	Gly	Ile	Asp	Ser	Tyr	Thr
2281				580					585					590		
2282																
2283	Cys	Ile	_	Asn	Pro	Gly	Tyr	Met	Gly	Ala	Ile	Cys	Ser	Asp	Gln	Ile
2284			595					600					605			
2285																
2286	Asp		Cys	Tyr	Ser	Ser	Pro	Cys	Leu	Asn	Asp	Gly	Arg	Cys	Ile	Asp
2287		610					615					620				
2288				_		_				_		_			_	
2289		Val	Asn	Gly	Tyr		Cys	Asn	Cys	Gln		Gly	Thr	Ser	Gly	
2290	625					630					635					640
2291		_			_		_	_		_ =		_				
2292	Asn	Cys	Glu	Ile		Phe	Asp	Asp	Cys		Ser	Asn	Pro	Cys	Ile	His
2293					645					650					655	
2294			_		_			_	_	_	_	_	<b>.</b>	_	_	_
2295	GГУ	Ile	Cys	Met	Asp	Gly	Ile	Asn	Arg	Tyr	Ser	Cys	Val	Cys	Ser	Pro

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2296				660					665					670		
2297			_,			_	_	_		_		_				
2298	GLY	Phe		Gly	GIn	Arg	Cys		Ile	Asp	Ile	Asp		Cys	Ala	Ser
2299			675					680					685			
2300	_	_		_	_	<b>-</b>							_		_	
2301	Asn		Cys	Arg	Lys	Gly		Thr	Cys	Ile	Asn	Gly	Val	Asn	Gly	Phe
2302		690					695					700				
2303			_			_										
2304		Cys	Ile	Cys	Pro		Gly	Pro	His	His		Ser	Cys	Tyr	Ser	Gln
2305	705					710					715					720
2306																
2307	Val	Asn	Glu	Cys		Ser	Asn	Pro	Cys		His	Gly	Asn	Cys		Gly
2308					725					730					735	
2309																
2310	Gly	Leu	Ser	Gly	Tyr	Lys	Cys	Leu	Cys	Asp	Ala	Gly	$\mathtt{Trp}$	Val	Gly	Ile
2311				740					745					750		
2312																
2313	Asn	Cys	Glu	Val	Asp	Lys	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Gln	Asn
2314			755					760					765			
2315																
2316	${ t Gly}$		Thr	Cys	Asp	Asn	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Thr	Cys	Lys
2317		770					775					780				
2318																
2319	Lys	Gly	Phe	Lys	Gly	Tyr	Asn	Cys	Gln	Val	Asn	Ile	Asp	Glu	Cys	Ala
2320	785					790					795					800
2321																
2322	Ser	Asn	Pro	Cys	Leu	Asn	Gln	Gly	Thr	Cys	Phe	Asp	Asp	Ile	Ser	Gly
2323					805					810					815	
2324																
2325	${ t Tyr}$	Thr	Cys	His	Cys	Val	Leu	Pro	Tyr	Thr	Gly	Lys	Asn	Cys	Gln	Thr
2326				820					825					830		
2327																
2328	Val	Leu		Pro	Cys	Ser	Pro		Pro	Cys	Glu	Asn		Ala	Val	Cys
2329			835					840					845			
2330				_										_		_
2331	Lys		Ser	Pro	Asn	Phe		Ser	Tyr	Thr	Cys		Cys	Ala	Pro	Gly
2332		850					855					860				
2333	_				_	_	_,		_		_		_		_	_
2334	-	GIn	GLY	Gln	Arg	-	Thr	Ile	Asp	He	-	GIu	Cys	Ile	Ser	-
2335	865					870					875					880
2336	_	_		_	· .		_	_		_				_	_	
2337	Pro	Cys	Met	Asn		GTA	ьeu	Cys	His		Thr	GIn	Gly	Ser	_	Met
2338					885					890					895	
2339	<b>~</b>	<b>~</b> 1	<b>~</b> .	D	D	<b>~</b> 1	D1 -	٥.	<b>~</b> 3	14:-1	<b>3</b>	<b>~</b>	<b>~</b> 3	<b>~</b> 3	<b>3</b> .	<b>~</b> 7
2340	cys	Glu	cys	Pro	Pro	GTA	Pne	ser	_	Met	Asp	cys	Glu		Asp	тте
2341				900					905					910		
2342	•		α.	<b>.</b>		<b>.</b>	ъ.	~	~ 7		<b>a</b> 7	<b>~</b> 7	•	<b>~</b>		_
2343	Asp	Asp		Leu	ата	Asn	Pro		GIN	Asn	GTA	GTA		cys	Met	Asp
2344			915					920					925			
2345	<b>~</b> 1-	77 T	7	m1	DI	<b>a</b>	<b>~</b>	<b>.</b>	<b>a</b> -	<b>.</b>	<b>5</b>	<b>~</b> 1	D)	m)	~ 3	
2346	σтУ	vaı	Asn	Thr	rne	ser	cys	ьeu	cys	ьeu	rro	θŢЙ	rne	Inr	GТĀ	Asp

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2347		930					935					940				
2348																
2349	Lys	Cys	Gln	Thr	Asp	Met	Asn	Glu	Cys	Leu	Ser	Glu	Pro	Cys	Lys	Asn
2350	945					950					955					960
2351																
2352	${ t Gly}$	Gly	Thr	Cys	Ser	Asp	Tyr	Val	Asn	Ser	Tyr	Thr	Cys	Lys	Cys	Gln
2353					965					970					975	
2354																
2355	Ala	Gly	Phe	Asp	Gly	Val	His	Cys	Glu	Asn	Asn	Ile	Asn	Glu	Cys	Thr
2356				980					985					990	-	
2357																
2358	Glu	Ser	Ser	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asp	Gly	Ile	Asn	Ser
2359			995	_			_	1000		_		_	1009			
2360																
2361	Phe	Ser	Cys	Leu	Cvs	Pro	Val	Glv	Phe	Thr	Glv	Ser	Phe	Cvs	Leu	His
2362		1010	-		-		101	_			- 1	1020		- 2		
2363			-													
2364	Glu	Ile	Asn	Glu	Cvs	Ser	Ser	His	Pro	Cvs	Leu	Asn	Glu	Glv	Thr	Cvs
2365	102				-7-	1030				0,70	103		0_0			1040
2366							•									1010
2367	Val	Asp	Glv	Leu	Glv	Thr	Tyr	Δrα	Cvs	Ser	Cvs	Pro	T.e.11	Glv	Tur	Thr
2368		1101			1045		- 7 -		Cys	1050			шси	Cry	105	
2369											•					-
2370	Glv	Lys	Δan	Cvs	Gln	Thr	T.e11	Val	Δen	T.e.11	Cve	Sar	Δrα	Sar	Dro	Cve
2371	CLY	цуБ	71011	1060			шси	vai	1069		Cys	JCI	AL 9	1070		Cys
2372				100	,				100.	,				107	,	
2372	Lvc	Asn	Tarc	C137	Thr	Cvc	<b>17</b> -1	Cln	Tara	Tara	ח ד ת	C1.,	802	~1 <sub>~</sub>	Crra	T 011
2374	цуз	VOII	107		1111	Cys	Val	1080	_	цуs	Ата	GIU	1085		Cys	пеп
2375			107	,				1000	,				108	•		
2376	C***	Dwo	Com	<b>~1</b>	П	77-	<b>~1</b>	77.	П	C	7	170 7	D	7	17-7	
	Cys	Pro		GIY	пр	AIA			TYL	Cys	Asp			ASII	vaı	ser
2377		1090	,				109	)				1100	J			
2378	G	7	T1.	77.	77.	0	7	7	<b>a</b> 1	77-7	T	**- 7	~1	TT 2	<b>.</b>	<b>G</b>
2379		Asp	тте	ALA	Ala		_	Arg	GIA	vaı			GIU	HIS	Leu	_
2380	1105	•				111(	,				1115	•				1120
2381	<b>~</b> 3.		_	~3		_		_		~-3	_	1	•	_	_	
2382	GIN	His	ser	GIY		_	тте	Asn	Ата	_		Thr	His	Tyr	_	
2383					1125	>				1130	)				1135	•
2384	~	_	_	~ 7	_		~7	_		_	~-7			_	_	
2385	Cys	Pro	Leu	_	_	Thr	GLY	Ser	_	_	GIu	GIu	GIn		_	GIu
2386				1140	)				1145	5				1150	)	
2387	_		_	_	_	_										
2388	Cys	Ala			Pro	Cys	GIn		_	Ala	Thr	Cys		_	Phe	Ile
2389			115	•				1160	)				1165	5		
2390			_	_	_		_		_		_					
2391	GLy	Gly	_	Arg	Cys	Glu	_		Pro	Gly	Tyr		-	Val	Asn	Cys
2392		1170	)				1179	5				1180	)			
2393																
2394			Glu	Val	Asp			Gln	Asn	Gln			Gln	Asn	Gly	Gly
2395	1185	5				1190	)				1199	5	•			1200
2396																
2397	Thr	Cys	Ile	Asp	Leu	Val	Asn	His	Phe	Lys	Cys	Ser	Cys	Pro	Pro	Gly

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2398					1209	5				121	0				121!	5
2399 2400	Thr	7. ~~	C1	T ou	T 011	C	~1	<b>~</b> 1	7 ~~	T1.	7 ~~	7. ~~	0	77.0	7	<b>G</b> 1
2400	1111	Arg	Gry	Leu 122		Cys	GIU	GIU	122		Asp	Asp	Cys		-	GIÀ
2401				122	,				122	5				123	J	
2402	Pro	Hic	Cve	Leu	λan	Glv	Glaz	Gln	Carc	Mot	λαn	7/ 2/2	Tlo	C111	C111	Ф. т.
2404	FIO	1112	123		POII	СТУ	Gry	1240	_	Mec	Asp	Arg	124	_	GIY	ıyı
2405			123	,				124	J				144	,		
2406	Ser	Cvs	Δrα	Cys	Len	Pro	Glv	Dhe	Δla	Glv	Glu	Δτα	Cve	Glu	Clv	Agn
2407	501	1250	_	Cyb	пси	110	125		niu	O <sub>T</sub> y	OIU	126	_	Gru	OLY	rob
2408		120	•				127.	,				120	O			
2409	Tle	Δsn	Glu	Cys	Len	Ser	Δan	Pro	Cvs	Ser	Ser	Glu	Glv	Ser	T.e.u	Agn
2410	126		GIU	Cyb	шси	1270		110	Cys	ber	127!		GTÅ	OCI	пси	1280
2411	120.	•									127.	,				1200
2412	Cvs	Tle	Gln	Leu	Thr	Δsn	Asn	Tyr	T.em	Cvs	Val	Cvs	Δrα	Ser	Δla	Phe
2413	Cys		· · · ·	Lea	1285		p	-1-	шси	129		Cyb	**** 9	501	129	
2414					120.	•				127	•				127.	,
2415	Thr	Glv	Ara	His	Cvs	Glu	Thr	Phe	Val	Asp	Val	Cvs	Pro	Gln	Met	Pro
2416		0-1		1300	_				130	_		0,0		1310		
2417															•	
2418	Cvs	Leu	Asn	Gly	Glv	Thr	Cvs	Ala	Val	Ala	Ser	Asn	Met	Pro	Asp	Glv
2419	-1-		131	-	1		-1-	1320					132			<b>-</b> -1
2420				_					_					_		
2421	Phe	Ile	Cvs	Arg	Cys	Pro	Pro	Glv	Phe	Ser	Gly	Ala	Arq	Cvs	Gln	Ser
2422		1330	_		•		1339	_			4	1340	_		-	
2423																
2424	Ser	Cvs	Gly	Gln	Val	Lys	Cvs	Arq	Lvs	Gly	Glu	Gln	Cys	Val	His	Thr
2425	134	-	_			1350	_		-	•	135!		-			1360
2426																
2427	Ala	Ser	Gly	Pro	Arg	Cys	Phe	Cys	Pro	Ser	Pro	Arg	Asp	Cys	Glu	Ser
2428			_		1369			-		1370		_	_	-	1379	
2429																
2430	Gly	Cys	Ala	Ser	Ser	Pro	Cys	Gln	His	Gly	Gly	Ser	Cys	His	Pro	Gln
2431				1380	)				138	5				1390	)	
2432																
2433	Arg	Gln	Pro	Pro	Tyr	Tyr	Ser	Cys	Gln	Cys	Ala	Pro	Pro	Phe	Ser	Gly
2434			139	5				1400	)				140	5		
2435																
2436	Ser	Arg	Cys	Glu	Leu	Tyr	Thr	Ala	Pro	Pro	Ser	Thr	Pro	Pro	Ala	Thr
2437		1410	)				1419	5				142	0			
2438																
2439	Cys	Leu	Ser	Gln	Tyr	Cys	Ala	Asp	Lys	Ala	Arg	Asp	Gly	Val	Cys	Asp
2440	142	5				1430	)				143	5				1440
2441																
2442	Glu	Ala	Cys	Asn			Ala	Cys	Gln			Gly	Gly	Asp		
2443					1445	5				145	כ				145	5
2444	_	_,			_	_	_		_		_	_	_	_	_	_
2445	Leu	Thr	Met	Glu		Pro	Trp	Ala		-	Ser	Ser	Pro			Cys
2446				1460	ט				146	5				1470	)	
2447	-	_	_		_	_	~ -	~	_	~-	_	~	_	_,		~ 7
2448	Trp	Asp	Tyr	Ile	Asn	Asn	GIn	Cys	Asp	Glu	Leu	Cys	Asn	Thr	val	GIU

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2449			1479	5				148	0				148	5		
2450																
2451	Cys	Leu	Phe	Asp	Asn	Phe	Glu	Cys	Gln	Gly	Asn	Ser	Lys	Thr	Cys	Lys
2452		1490					149			-		150			-	-
2453										v						
2454	Tyr	Asp	Lys	Tyr	Cys	Ala	Asp	His	Phe	Lys	Asp	Asn	His	Cvs	Asn	Gln
2455	150!		-	-	-	1510	_			-	151			-		1520
2456																
2457	Gly	Cys	Asn	Ser	Glu	Glu	Cys	Gly	Trp	Asp	Gly	Leu	Asp	Cys	Ala	Ala
2458	-	•			152		•	•	•	153	_		-	-	153	
2459																
2460	Asp	Gln	Pro	Glu	Asn	Leu	Ala	Glu	Glv	Thr	Leu	Val	Ile	Val	Val	Leu
2461	-			1540					154					155		
2462															_	
2463	Met	Pro	Pro	Glu	Gln	Leu	Leu	Gln	Asp	Ala	Ara	Ser	Phe	Leu	Ara	Ala
2464			155					156	_				156		5	
2465									-					-		
2466	Leu	Gly	Thr	Leu	Leu	His	Thr	Asn	Leu	Ara	Ile	Lvs	Ara	Asp	Ser	Gln
2467		1570					1575			3		1580				<del></del>
2468								-					-			
2469	Gly	Glu	Leu	Met	٧al	Tyr	Pro	Tvr	Tvr	Glv	Glu	Lvs	Ser	Ala	Ala	Met
2470	158					1590		- 4 -	- 2 -	2	159	_				1600
2471																
2472	Lvs	Lys	Gln	Ara	Met	Thr	Ara	Ara	Ser	Leu	Pro	Glv	Glu	Gln	Glu	Gln
2473	4	4		,	1609		5	3		1610		1			161	
2474											_					-
2475	Glu	Val	Ala	Glv	Ser	Lvs	Val	Phe	Leu	Glu	Ile	Asp	Asn	Ara	Gln	Cys.
2476				1620		2			162					1630		-7-
2477										-						
2478	Val	Gln	Asp	Ser	Asp	His	Cvs	Phe	Lvs	Asn	Thr	Asp	Ala	Ala	Ala	Ala
2479			163				-1-	1640	_			E	164!			
2480				-												
2481	Leu	Leu	Ala	Ser	His	Ala	Ile	Gln	Glv	Thr	Leu	Ser	Tvr	Pro	Leu	Val
2482		1650					165		2			1660	_			
2483																
2484	Ser	Val	Val	Ser	Glu	Ser	Leu	Thr	Pro	Glu	Arq	Thr	Gln	Leu	Leu	Tvr
2485	1669					1670					167					1680
2486																
2487	Leu	Leu	Ala	Val	Ala	Val	Val	Ile	Ile	Leu	Phe	Ile	Ile	Leu	Leu	Gly
2488					1689					1690					169	_
2489																
2490	Val	Ile	Met	Ala	Lys	Arq	Lys	Arq	Lvs	His	Gly	Ser	Leu	Trp	Leu	Pro
2491				1700		_	•		170		-			1710		
2492																
2493	Glu	Gly	Phe	Thr	Leu	Arg	Arq	Asp	Ala	Ser	Asn	His	Lys	Arq	Arq	Glu
2494		•	1715					1720		·			172	-	J	
2495																
2496	Pro	Val	Gly	Gln	Asp	Ala	Val	Gly	Leu	Lys	Asn	Leu	Ser	Val	Gln	Val
2497		1730			-		1739	_		-		1740				
2498																
2499	Ser	Glu	Ala	Asn	Leu	Ile	Gly	Thr	Gly	Thr	Ser	Glu	His	${\tt Trp}$	Val	Asp

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2500	774	_				175/						_				7.77.0
2500 2501	1745	•				1750	J				1755	•				1760
2502	7 cn	Glu	C111	Dro	Cln	Dro	Tara	Tara	1701	Tura	ח ה	C1.,	7 00	C1	. ד ת	T 011
2503	Asp	Giu	GTĀ	PIO	1765		цуъ	цуз	vai	1770		GIU	Asp	Gru	1775	
2504					1/05	,				1//	,				1//:	•
2505	Len	Sar	Glu.	Gl 11	Λαn	7 cm	Dro	Tla	Λαn	λνα	7 ~~	Dro	Trn	Thr	Cln	Cln.
2506	пец	Ser	GIU	1780	_	Asp	PIO	116	1789	_	Arg	PLO	пр	1790		GIII
2507				1/00	,				1/0:	,				1/30	,	
2508	Uic	Leu	Glu.	Nla	Nlα	Λαn	Tla	7 20	722	Thr	Dro	Cor	T 011	ת דת	T 011	Thr
2509	1115	пец	179		AIG	тэр	116	1800	_	IIII	PIO	261	1805		пец	1111
2510			1/).	,				1000	,				100.	,		
2511	Pro	Pro	Gln	Δla	Glu	Gln	Glu	Va l	Aan	V-1	T.011	λαη	Val	λan	Val	7 ra
2512	FIO	1810		ALG	GIU	GIII	181		тэр	vai	пец	1820		Poli	val	Arg
2512		1010	,				101.	,				102	,			
2514	Glaz	Pro	λen	Glv	Cve	Thr	Dro	T.011	Mot	T.011	בומ	Sar	T.A11	Δνα	Glv	Gl v
2515	1825		nop	Cry	Cyb	1830		ЦСи	1100	Lea	1835		шси	AL 9	Cly	1840
2516	1025					105	,				105.	•				1040
2517	Ser	Ser	Δan	T.e.11	Ser	Δen	Glu	Agn	G] 11	Δen	בומ	Glu	Agn	Sar	Sar	בומ
2518	UC_	001	пор	LCu	1845	_	OIU	ממני	014	1850		014	nop	UCI	1855	
2519						•				1050	•				105.	•
2520	Δsn	Ile	Tle	Thr	Asn	Leu	Val	Tur	Gln	Glv	Δla	Ser	T.em	Gln	Δla	Gln
2521	11011			1860	_	Leu	Vul	- 7 -	1865	_	1114		шси	1870		0.1.1.
2522					•										•	
2523	Thr	Asp	Ara	Thr	Glv	Glu	Met	Δla	Len	His	Len	Ala	Δla	Ara	Tvr	Ser
2524			187		<b>U</b> -1			1880		1120			1885	_	-1-	001
2525			<b></b> _,	•				1000	•					•		
2526	Ara	Ala	Asp	Δla	Δla	Lvs	Ara	Leu	Len	Asp	Δla	Glv	Δla	Asp	Δla	Asn
2527		1890	_			-1-	189			пор		1900			****	11011
2528			•										•			
2529	Άla	Gln	Asp	Asn	Met	Glv	Ara	Cvs	Pro	Leu	His	Ala	Ala	Val	Ala	Ala
2530	1905		p			1910	_	0,0			1915					1920
2531																
2532	Asp	Ala	Gln	Glv	Val	Phe	Gln	Ile	Leu	Ile	Ara	Asn	Ara	Val	Thr	Asp
2533	•			4	1925					1930	_		,		1935	_
2534																
2535	Leu	Asp	Ala	Arq	Met	Asn	Asp	Gly	Thr	Thr	Pro	Leu	Ile	Leu	Ala	Ala
2536		-		1940			-	•	1945					1950		
2537																
2538	Arg	Leu	Ala	Val	Glu	Gly	Met	Val	Ala	Glu	Leu	Ile	Asn	Cys	Gln	Ala
2539	_		195			-		1960					1965	_		
2540																
2541	Asp	Val	Asn	Ala	Val	Asp	Asp	His	Gly	Lys	Ser	Ala	Leu	His	Trp	Ala
2542		1970	)				197	5				1980	)			
2543																
2544	Ala	Ala	Val	Asn	Asn	Val	$\operatorname{Glu}$	Ala	Thr	Leu	Leu	Leu	Leu	Lys	Asn	Gly
2545	1985					1990					1995					2000
2546																
2547	Ala	Asn	Arg	Asp	Met	Gln	Asp	Asn	Lys	Glu	Glu	Thr	Pro	Leu	Phe	Leu
2548					2005	5				2010	)				2015	5
2549																
2550	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Ala	Ala	Lys	Ile	Leu	Leu	Asp	His

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2551				2020	0				202	5				203	)	
2552			_	_	_								_			
2553	Phe	Ala			Asp	Ile	Thr			Met	Asp	Arg	Leu		Arg	Asp
2554			203	5				2040	)				2045	5		
2555	_	_								_	_					_
2556	Val		_	Asp	Arg	Met			Asp	Ile	Val	Arg	Leu	Leu	Asp	Glu
2557		2050	)				205	5				2060	)			
2558																
2559	Tyr	Asn	Val	Thr	Pro	Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	Ala	Leu
2560	206	5				2070	כ				207	5				2080
2561																
2562	Ser	Pro	Val	Ile	Cys	Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	Lys	His
2563					208	5				2090	)				2095	5
2564																
2565	Thr	Pro	Met	Gly	Lys	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met
2566				2100	_	-		_	210				_	2110		
2567																
2568	Pro	Thr	Ser	Leu	Pro	Asn	Leu	Ala	Lvs	Glu	Ala	Lvs	Asp	Ala	Lvs	Glv
2569			211!					2120				-1-	2125		-1-	~-1
2570								~~~								
2571	Ser	Ara	Δrα	Lvs	Lvs	Ser	T.e.ii	Ser	Glu	Lvs	Val	Gln	Leu	Ser	Glu	Ser
2572	JCI	2130	_	2,5	270	JUL	213		014	<b></b> ,	val	2140		501	014	001
2573		213	,				213.	,				411	,			
2574	Sar	Val	Thr	T.211	Sar	Pro	T = T	Λen	Sar	T.011	Glu	Sor	Pro	uic	Thr	Тугт
2575	214!		1111	пец	261	2150		Asp	261	пец	215!		FIO	1113	1111	2160
2576	214:	,				213(	,				210	,				2100
2577	Lov	Com	7 ~~	The	mb w	Cox	Cor	Deco	Mot	T1.	The	Com	Dwo	<b>a</b> 1	т1.	T 011
2578	vai	261	Asp	TIIT			Set	PIO	Met			ser	Pro	GIĀ		
					2169	•				2170	J				2179	•
2579	<b>~</b> 1	<b>7</b> .7 –	<b>a</b>	D	7	D	3.7 - L	<b>T</b>	n 1 -	m1	77-	<b>77</b> -	D	D	<b>77</b> -	D
2580	GIII	Ala	ser			Pro	Met	ьeu			Ата	ALA	Pro			Pro
2581				2180	J				218	)				2190	,	
2582	77-7	77.º	77-	<b>G</b> 1	77.	77-	<b>.</b>	<b>a</b>	D1		3	<b>.</b>	*** _	<b>~</b> 1		<b>~</b> 1
2583	vai	HIS			HIS	Ala	Leu			ser	ASI	Leu	His		Met	GIN
2584			219	•				2200	J				2205	)		
2585	<b>5</b>				<b>a</b> 1					_	-	~		~	~1	<b>-</b> .
2586	Pro			HIS	GIY	Ата			vaı	ьeu	Pro		Val	Ser	GIn	ьeu
2587		2210	)				221	>				2220	י			
2588	_	_		•				_	_	~-7	_	~-7	_	_ ,	~-7	_
2589			His	His	His			Ser	Pro	Gly		_	Ser	Ala	GIY	
2590	222	5				2230	)				223	5				2240
2591							_		_		_					
2592	Leu	Ser	Arg	Leu			Val	Pro	Val			Asp	$\mathtt{Trp}$	Met		_
2593					2245	5				2250	)				225	5
2594		_	_		_	_	_			-		_	_		_	
2595	Met	Glu	Val			Thr	Gln	Tyr			Met	Phe	Gly			Leu
2596				2260	0				226	5				2270	)	
2597																
2598	Ala	Pro	Ala	Glu	Gly	Thr	His	Pro	Gly	Ile	Ala	Pro	Gln	Ser	Arg	Pro
2599			2275	5				2280	)				2285	5		
2600																
2601	Pro	Glu	Gly	Lys	His	Ile	Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile

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2602	2290		2295		230	0	
2603	mlass plans Glass	T T3 -	D	<b>~</b> 3 ~ <b>~</b>	-1 - 11	a1 n	
	Thr Phe Gln		_	GIY Ser		GIn Pro	-
2605 230	5	2310	)		2315		2320
2606	D 01- D	<b>61</b> 6	m1 a	<b>5 5</b>		~-	
	Pro Gln Pro		Thr Cys			. Ala Gly	
2608		2325		233	U		2335
2609	Mlass Mata Massa	G1 T1-	D-10 Gl.	N 77-	3 T	. D 0	**-1 71-
	Thr Met Tyr		Pro Giu		Arg Let		
2611	2340	)		2345		235	U
2612	Dee Mha Nia	M-+ M-+	D 01	G] 3	al al	77-7 77-	Olas Mhas
	Pro Thr Ala	met met			GIA GIL		Gin Thr
2614	2355		236	U		2365	
2615	T D 31-	m 11 -	Desc. Dies	D 21-	G 17-1	G] T	D
	Leu Pro Ala	Tyr His		Pro Ala			Tyr Pro
2617	2370		2375		238	0	
2618	Desa Desa Casa	G] - TI -	G	37- 0	G 7		<b>0</b> 1 <b>3</b>
	Pro Pro Ser			Ala Ser		AIA AIA	
2620 238	5	2390	,		2395		2400
2621	Des Con III	C Cl	114 m T a	01- 01-		D-15 (T-11	Tau Mha
2622 Thr 2623	Pro Ser His	_	HIS Leu	<del>-</del>		Pro Tyr	
2624		2405		241	U		2415
	Cor Dro Clu	Cor Dro	Aan Cln	Two Com	Com Cor	Com Dwo	Hia Com
2625 PIO	Ser Pro Glu 2420		ASP GIII	2425	ser ser		
2627	2420	,		2425		243	
	Ser Asp Trp	Ser Asn	Wal Thr	Thr Car	Dro Thr	Pro Cly	י אום.
2629 A1a	2435	ser Asp	244		PIO III	2445	GIY AIA
2630	2433		211	O		2443	
	Gly Gly Gln	Ara Gly	Pro Gly	Thr Hie	Met Ser	Glu Pro	Dro Hie
2632	2450	Arg Cry	2455	1111 1113	246		FIO IIIS
2633	2150		2133		210		
	Asn Met Gln	Val Tvr	Ala				
2635 246		2470					
2636							
	RMATION FOR S	SEO ID NO	0:20:				
2638		~					
2639 (i)	SEQUENCE CHA	RACTERIS	STICS:				
2640	(A) LENGTH:			ds '			
2641	(B) TYPE: a		_				
2642	(C) STRANDE	EDNESS: s	single				
2643	(D) TOPOLOG		_				
2644							
2645 (ii)	MOLECULE TYP	E: pepti	de				
2646		- <b>-</b>					
2647							
2648							
2649 (xi)	SEQUENCE DES	CRIPTION	: SEQ I	D NO:20:		•	
2650							
	Pro Pro Leu		Pro Leu	Leu Cys	Leu Ala	Leu Leu	
2652 1		5		10			15

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2653																
2654	Leu	Ala	Ala	Arq	Gly	Pro	Ara	Cvs	Ser	Gln	Pro	Glv	Glu	Thr	Cvs	Leu
2655				20	•		Ĭ	-	25			•		30	•	
2656																
2657	Asn	Gly	Gly	Lys	Cys	Glu	Ala	Ala	Asn	Gly	Thr	Glu	Ala	Cys	Val	Cvs
2658		•	35	•	•			40		-			45	- 2		-1-
2659																
2660	Glv	Glv	Ala	Phe	Val	Glv	Pro	Ara	Cvs	Gln	Asp	Pro	Asn	Pro	Cvs	Len
2661	1	50				1	55	3	-2-			60			-7.	
2662							-					•				
2663	Ser	Thr	Pro	Cvs	Tays	Δsn	Δla	Glv	Thr	Cve	Hig	Val	Val	Δen	Δrα	Ara
2664	65			<b>-7.</b>	_,_	70	1114			CID	75		· · · ·	1101	9	80
2665	0.5					, 0					, 5					00
2666	Glaz	Val.	Δla	Aen	ጥኒም	Δla	Cve	Sar	Cve	70.70	T.011	G137	Phe	Sar	Glar	Dro
2667	GLY	vai	лια	App	85	лта	Суз	SCI	Cys	90	пец	GLY	FIIC	261	95	FIO
2668					0,5					50					93	
2669	T 011	Cara	T 011	Thr	Dro	T 011	7 00	7 0 0	ח ד ת	Crra	T 011	The	7 ~~	Dwo	C1.0	7
2670	цец	Суб	пец	100	PIO	ьeu	Asp	ASII	105	Cys	пеп	1111	Asn		Cys	Arg
2671				100					103					110		
2672	7 00	~1	<i>α</i> 1	mb ~	Crra	7 ~~	T 011	T 0	The	T 011	The	<i>~</i> 1	TT+	T	C	7
2673	ASII	GLY	_	1111	Cys	Asp	Leu		THE	ьец	IIII	GIU	Tyr	ьуѕ	Cys	Arg
2674			115					120					125			
	<b>G</b>	Deep	Dece	a1	Mana	0	a1	T	C	a	<b>01</b>	a1	77-	7	D	G
2675	Cys		Pro	GTA	пр	ser	-	ьуs	ser	Cys	GIII		Ala	Asp	Pro	Cys
2676		130					135					140				
2677	77-	<b>0</b>	7	D	<b>G</b>	7.7.	7	<b>~</b> 1	<b>~</b> 1	<b>~</b> 1	<b>a</b>	<b>.</b>	D	D1	<b>a1</b>	
2678		ser	Asn	Pro	Cys		Asn	GIY	GIY	GIN	_	Leu	Pro	Pne	GIU	
2679	145					150					155					160
2680	_	_		_		_	_	_	_	_,		~-	_	_,	_	_
2681	ser	Tyr	тте	Cys		Cys	Pro	Pro	Ser		His	GIA	Pro	Thr	_	Arg
2682					165					170					175	
2683		_		_					_	_	_	_	_	_		
2684	GIn	Asp	Val		GLu	Cys	Gly	GIn	_	Pro	Arg	Leu	Cys	_	His	GIA
2685				180					185					190		
2686			_		_				_		_	_		_	_	
2687	Gly	Thr	_	His	Asn	Glu	Val	_	Ser	Tyr	Arg	Cys	Val	Cys	Arg	Ala
2688			195					200					205			
2689	_	_	_	_				_								
2690	Thr		Thr	Gly	Pro	Asn	_	Glu	Arg	Pro	Tyr		Pro	Cys	Ser	Pro
2691		210					215					220				
2692																
2693		Pro	Cys	Gln	Asn	Gly	Gly	Thr	Cys	Arg		Thr	Gly	Asp	Val	Thr
2694	225					230					235					240
2695																_
2696	His	Glu	Cys	Ala	Cys	Leu	Pro	Gly	Phe		Gly	Gln	Asn	Cys		Glu
2697					245					250					255	
2698																
2699	Asn	Ile	Asp	Asp	Cys	Pro	Gly	Asn	Asn	Cys	Lys	Asn	Gly	Gly	Ala	Cys
2700				260					265					270		
2701																
2702	Val	Asp	Gly	Val	Asn	Thr	Tyr	Asn	Cys	Pro	Cys	Pro	Pro	Glu	Trp	Thr
2703			275					280					285			

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2704																
2705	Gly	Gln	Tyr	Cys	Thr	Glu	Asp	Val	Asp	Glu	Cvs	Gln	Leu	Met	Pro	Asn
2706	-	290	•	•			295		•		•	300				
2707																
2708	Ala	Cys	Gln	Asn	Gly	Gly	Thr	Cys	His	Asn	Thr	His	Gly	Gly	Tyr	Asn
2709	305	-			-	310		4			315		- 4	2	- 2 -	320
2710																
2711	Cvs	Val	Cvs	Val	Asn	Glv	Tro	Thr	Glv	Glu	Asp	Cvs	Ser	Glu	Asn	Ile
2712	- 2		- 1		325	2			1	330	<b>F</b> -	-1-			335	
2713															555	
2714	Asp	Asp	Cvs	Ala	Ser	Ala	Ala	Cvs	Phe	His	Glv	Δla	Thr	Cvs	His	Asp
2715			07.5	340	202			0,0	345		0-1			350		1101
2716				310					313					330		
2717	Δνα	Val	Δla	Ser	Dhe	Tur	Cve	Glu	Cve	Pro	Hie	Glv	Δνα	Thr	Glv	T.e.ii
2718	A. g	Val	355	JCI	1110	- y -	Cys	360	Cys	110	1115	Gry	365	1111	GLY	Бец
2719			333					300					303			
2720 .	T.011	Cve	Uic	Leu	λen	Λen	λla	Cvc	Tla	Sar	λan	Dro	Cvc	λan	Glu	Gl v
2721	шец	370	1113	пец	ASII	ASP	375	Cys	TTC	Ser	ASII	380	Cys	ASII	GIU	Gry
2722		3/0					3/3					360				
2723	Sor	λαn	Cara	7) cm	Thr	7 an	Dro	7707	7 an	Clar	Tara	ח ה	T1.	Crra	Thr	Caro
2724	385	ASII	Cys	Asp	1111	390	PIO	vaı	ASII	GIY	395	Ата	TTE	Cys	1111	_
2725	363					390					333					400
	Dwo	Com	<b>~1</b>	TT	Tha	a1	Dwo	77.	a	Com	<u>ما -</u>	7 ~~	1707	7 ~~	a1	<b>a</b>
2726	PFO	ser	GIY	Tyr		GIĀ	PIO	AId	Cys		GIII	Asp	vai	Asp		Cys
2727					405					410					415	
2728	0	T	<b>~1</b>	77-	7	D	G	<b>~1</b>	TT-2	77-	<b>a</b> 1	T	<b>~</b>	<b>T1</b> -	7	ml
2729	ser	Leu	GIY	Ala	ASII	Pro	Cys	GIU		Ala	GIY	ьуѕ	Cys		ASII	Thr
2730				420					425					430		
2731		~1	<b>.</b>	<b>5</b> 1	~1	~	<b>~</b> 1	<b>~</b> .	-	<b>~</b> 1	<b>~</b> 1	_	en)	<b>~</b> 3	_	_
2732	Leu	GLY		Phe	GIU	Cys	GIN	_	Leu	GIn	GLY	Tyr		GIY	Pro	Arg
2733			435					440					445			
2734	~	<b>~</b> 1	-1.		**- 7		~1	~					~	~7		_
2735	Cys		тте	Asp	vaı	Asn		Cys	vaı	ser	Asn		Cys	Gin	Asn	Asp
2736		450					455					460				
2737		<b>1</b>	~	_	_	~7		<b>~</b> 1	~1	-1	<b>~</b> 1	~		_		_
2738		Thr	Cys	Leu	Asp		тте	GTA	GIU	Pne		Cys	Met	Cys	Met	
2739	465					470					475					480
2740	~-7	_	~-7	~-7			_	~ 7		_	_,	_	~-1	_		-
2741	GLY	Tyr	GIu	Gly		His	Cys	GIu	Val		Thr	Asp	GIu	Cys		Ser
2742					485					490					495	
2743	_	_		_		_		_		_	_	_		_		
2744	Ser	Pro	Cys	Leu	His	Asn	Gly	Arg	_	Leu	Asp	Lys	Ile		Glu	Phe
2745				500					505					510		
2746	<b>-</b>	_	<b>-</b>	_	_							_	_		_	_
2747	Gln	Cys		Cys	Pro	Thr	Gly		Thr	Gly	His	Leu	-	Gln	Tyr	Asp
2748			515					520					525			
2749																
2750	Val		Glu	Cys	Ala	Ser		Pro	Cys	Lys	Asn	_	Ala	Lys	Cys	Leu
2751		530					535					540				
2752	_		_	_		_		_		_				_		
2753	_	Gly	Pro	Asn	Thr	_	Thr	Cys	Val	Cys		Glu	Gly	Tyr	Thr	_
2754	545					550					555					560

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2755																
2756	Thr	His	Cvs	Glu	Val	Asp	Ile	Asp	Glu	Cvs	Asp	Pro	Asp	Pro	Cvs	His
2757					565					570					575	
2758																
2759	Tyr	Gly	Ser	Cys	Lys	Asp	Glv	Val	Ala	Thr	Phe	Thr	Cys	Leu	Cvs	Ara
2760	-	2		580			1		585				-1-	590	-1-	5
2761																
2762	Pro	Glv	Tvr	Thr	Glv	His	His	Cvs	Glu	Thr	Asn	Tle	Asn	Glu	Cvs	Ser
2763		1	595		1			600					605		0,0	
2764													000			
2765	Ser	Gln	Pro	Cvs	Ara	Len	Ara	Glv	Thr	Cvs	Gln	Δan	Pro	Agn	Δen	Δla
2766		610		<b>C</b> 15		Lea	615	O±y		Cyb	0111	620	110	HOP	ASII	niu
2767		010					013					020				
2768	Тух	T.e.11	Cvc	Dhe	Cve	T.e.ii	Lvc	G] v	Thr	Thr	Gl v	Dro	Asn	Cve	G111	Tla
2769	625	шси	Cys	1110	Cys	630	цуб	Ory	+11+	1111	635	110	ASII	Cys	Giu	640
2770	025					050					033					040
2771	Λen	Lou	λαn	λαn	Cvc	ת 1 ת	Car	Car	Dro	Cvc	7 an	Cor	Gly	Thr	Cva	T 011
2772	ASII	цец	Asp	Asp	645	Ата	Ser	Ser	PIO	650	Asp	per	СТУ	TIIT	655	пеп
2772					043					050					000	
2774	7.00	Tara	T1.	7.00	C1	TT	C1	C++0	ח ד ת	Crra	<b>~</b> 1	Dwo	<b>01</b>	M	The se	<b>a</b> 1
	Asp	ьуѕ	TTE	_	GIY	IÀT	GIU	Cys		Cys	GIU	PIO	Gly	_	1111	GIY
2775 2776				660					665					670		
	C	N/a+	<i>a</i>	7 ~~	0	7	T1.	7	<b>01</b>	a	77-	a1	7	D	<b>~</b>	TT-1
2777	ser	Mec	_	ASII	ser	ASII	ire	_	GIU	Cys	Ата	GIY	Asn	Pro	Cys	HIS
2778			675					680					685			
2779	<b>3</b>	<b>~</b> 1	<b>a</b> 1	m1	<b>a</b>	<b>a</b> 1	•	<b>~</b> 1	<b>#</b> 7.	•	<b>0</b> 1	<b>5</b> 1	cm1	~		~
2780	Asn	_	GIA	Thr	Cys	GIU	_	GIY	тте	Asn	GIY		Thr	Cys	Arg	Cys
2781		690					695					700				
2782	_	~7	~ 7	_	'	_	_	_,	_	_	_			_		_
2783		GIu	GIY	Tyr	His		Pro	Thr	Cys	Leu		GIu	Val	Asn	GIu	-
2784	705					710					715					720
2785	_	_	_	_	~			~3		_	_	_	_	_	_	
2786	Asn	Ser	Asn	Pro		vaı	His	GLY	Ala	_	Arg	Asp	Ser	Leu		GLY
2787					725					730					735	
2788		_	_	_	_	_	_		_	_		_,	_	_	_	
2789	Tyr	гàг	Cys	_	Cys	Asp	Pro	GIY	_	ser	GIY	Thr	Asn	_	Asp	IIe
2790				740					745					750		
2791	_	_	_		_	~7	_	_	_	_		_ ;		~-3		_
2792	Asn	Asn		GIu	Cys	GIu	Ser		Pro	Cys	Val	Asn	Gly	GTÅ	Thr	Cys
2793			755					760					765			
2794	_	_			_				_		_	_				_
2795	Lys		Met	Thr	Ser	GTA		Val	Cys	Thr	Cys	_	Glu	GIY	Phe	Ser
2796		770					775					780				
2797		_	_	_			_		_		_		_	_	_	_
2798	-	Pro	Asn	Cys	GIn		Asn	Ile	Asn	GLu	_	Ala	Ser	Asn	Pro	- <del>-</del> -
2799	785					790					795					800
2800	_	_	_			_		_	_						_	_
2801	Leu	Asn	Lys	GŢŸ		Cys	Ile	Asp	Asp		Ala	Gly	Tyr	Lys	_	Asn
2802					805					810					815	
2803	_	_	_	_	_		<b>_</b>				<b>-</b>			_		_
2804	Cys	Leu	Leu		Tyr	Thr	Gly	Ala		Cys	Glu	Val	Val		Ala	Pro
2805				820					825					830		

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Cys Ala Pro   Ser Pro   Cys Arg Asn Gly Gly Glu Cys Arg Gln   Ser Glu   Ser	2806																
2808		Cvs	Δla	Pro	Ser	Pro	Cvs	Ara	Asn	Glv	Glv	Glu	Cvs	Δτα	Gln	Ser	Glu
2810 2810 2811 2812 2813 2814 2815 2815 2816 2817 2816 2816 2816 2817 2817 2817 2818 2819 2816 2816 2817 2818 2819 2816 2817 2818 2819 2819 2810 2819 2810 2810 2811 2812 2811 2812 2812 2816 2816 2817 2828 2817 2828 2818 2819 2819 2819 2810 2820 2821 2821 2822 2820 2821 2822 2820 2821 2822 2820 2821 2822 2822		0,10					0,0	9		017		014	Cys		<b>Q</b> 111	001	O.L.u
Asp Tyr Glu Ser Phe Ser Cys Val Cys Pro Thr Ala Gly Ala Lys Gly 850									010					015			
2811		Asn	Tyr	Glu	Ser	Phe	Ser	Cve	Val	Cve	Pro	Thr	Δla	Glv	Δla	Lve	Gl v
2812 2813 2814 2815 2814 865 2816 886 8870 8875 8875 8880 2815 2816 2816 2816 2816 2817 2818 2819 2819 3810 3810 3817 2818 2819 3810 3817 2818 2819 3810 3810 3817 2818 2819 3810 3810 3817 3818 2819 3810 3810 3817 3818 3819 3810 3817 3818 3819 3810 3817 3818 3819 3819 3810 3817 3818 3819 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3819 3810 3811 3811 3819 3810 3811 3811 3811 3811 3811 3811 3811		p	_	014			501	_	val	Cyb		****		O <sub>T</sub> y	miu	5 ر	Cly
2813   Sin Thr Cys Glu Val   Spr Ile   Asn Glu Cys   Val   Leu   Ser   Pro   Cys   Arg   880			030					033					000				
2814   865		Gln	Thr	Cve	Glu	T = T	7 cn	Tla	Λan	Glu	Cvc	Val	Len	cor	Dro	Caro	71 200
2815 2816 2816 2817 2818 2819 2819 3815 2819 3816 2819 3816 2819 3817 3818 2819 3817 3818 2819 3817 3818 2819 3817 3818 2819 3819 3817 3818 2819 3819 3817 3818 2819 3819 3817 3818 2819 3819 3817 3818 2819 3818 2819 3819 3810 3810 3811 3818 3819 3818 3819 3818 3819 3818 3819 3818 3819 3818 3819 3818 3819 3818 3819 3818 3819 3818 3819 3818 3818			1111	Cys	Giu	vai	_	116	ASII	Gru	Суз		пеп	PET	PIO	Cys	_
2816   2817   2818   2819   2818   2819   2819   2819   2819   2819   2819   2819   2819   2820   2820   2821   2822   2822   2822   2825   2824   2825   2826   2827   2828   2828   2828   2828   2828   2828   2829   2826   2829   2826   2827   2828   2829   2826   2829   2827   2828   2829   2827   2828   2829   2828   2829   2829   2829   2829   2831   2829   2831   2829   2831   2829   2836   2828   2836   2829   2836		005					0 / 0					6/5					880
2817 2818 2819 2819 3819 3810 3817 3818 2819 3810 3817 3818 3817 3818 3817 3818 3819 3818 3819 3818 3819 3818 3819 3818 3819 3818 3819 3818 3818		ui a	C111	71-	802	Cara	C1 n	7 an	Thr	цiа	C1	C1	Ф	7 ~~~	Crra	TI-1 a	Crra
2818 2819 2819 2810 2820 2821 2822 2821 2822 2823 2915 2915 2824 2825 2826 2826 2827 2828 2827 2828 2827 2828 2829 2945 2829 2945 2829 2945 2829 2830 2831 2831 2831 2832 2834 2835 2834 2835 2836 2837 2838 2834 2837 2838 2834 2837 2838 2834 2837 2838 2834 2837 2838 2834 2835 2834 2835 2836 2837 2838 2834 2836 2837 2838 2834 2836 2837 2838 2834 2836 2837 2838 2836 2837 2838 2836 2837 2838 2837 2838 2838 2839 2840 2840 2840 2840 2840 2840 2840 2840		птэ	GTA	Ата	ser		GIII	ASII	1111	птъ		СТУ	туг	Arg	Cys		Cys
Sin Ala Gly Tyr Ser Gly Arg Asn Cys Glu Thr Asp Ile Asp Asp Cys 2820   910   900   905   910   910   910   920   910   920   910   920   910   920   920   920   925						005					090					095	
2820		<b>~1</b>	7.7.	<b>~1</b>	Ш	C	<b>a</b> 1	7	7	<b>G</b>	<b>a</b> 1	m1	7	<b>-</b> 1 -	7	7	<b>C</b>
2821 2822 Arg Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn 2823 915 925 925 925 925 925 925 925 925 925 92		GIII	Ата	GIY		ser	GTA	Arg	ASII	_	GIU	THE	Asp	iie	_	Asp	Cys
Arg   Pro   Asn   Pro   Cys   His   Asn   Gly   Gly   Ser   Cys   Thr   Asp   Gly   Ile   Asn   Pro   2823   915   925					900					905					910		
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2824 2825 Thr Ala Phe Cys Asp Cys Leu Pro Gly Phe Arg Gly Thr Phe Cys Glu 2826 930 935 940  2827  2828 Glu Asp Ile Asn Glu Cys Ala Ser Asp Pro Cys Arg Asn Gly Ala Asn 2829 945 950 955 960  2831 Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly Phe 2832 965 980 985 980  2834 Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser 2835 980 985 990  2836 Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys 2838 995 1000 1005  2839 2839  2840 Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val Asn 2841 1010 1015 1020  2842 2843 Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly 2844 1025 1030 1035 1040  2845 Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn 2846 Arg Gly Leu His Arg Cys Thr Cys Asp Ser Ser Pro Cys Lys Asn Gly 2850 1060 1065 1070  2851 1075 1080 1085  2852 Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val		Arg	Pro		Pro	Cys	His	Asn	-	GIY	ser	Cys	Thr	_	GIY	тте	Asn
## The Ala Phe Cys Asp Cys Leu Pro Gly Phe Arg Gly Thr Phe Cys Glu 930				915					920					925			
2826       930       935       940         2827       Glu Asp Ile Asn Glu Cys Ala Ser Asp Pro Cys Arg Asn Gly Ala Asn 229       945       950       955       960         2830       Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly Phe 2832       965       970       970       975       975         2833       Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser 980       985       990       990       990         2837       Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys 995       1000       1005       1005         2838       995       1000       1005       1005       1005         2841       1010       1015       1020       1020         2842       2843       Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly 1040       1035       1040         2844       1025       1030       1035       1040         2845       Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn 1045       1055       1055         2848       Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asp Gly 1065       1070       1055         2848       Cys Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser 1085       1085       1085		_,			_	_	_	_	_			_				_	
2827 2828     Glu Asp Ile Asn Glu Cys Ala Ser Asp Pro Cys Arg Asn Gly Ala Asn 2829     945     950     955     960  2830  2831     Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly Phe 2832     965     970     975  2833  2834     Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser 2835     980     985     990  2836  2837     Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys 2838     995     1000     1005  2839  2840     Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val Asn 2841     1010     1015     1020  2842  2843     Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly 2844     1025     1030     1035     1040  2845  2846     Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn 2847     1045     1050     1055  2851  2862     Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser 2853     1075     1080     1085  2855     Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val		Thr		Phe	Cys	Asp	Cys		Pro	Gly	Phe	Arg	_	Thr	Phe	Cys	Glu
Cys   Cys			930					935					940				
2829       945       950       955       960         2831       Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly Phe       965       970       975         2832       965       970       975       975         2833       Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser       980       985       985       990         2836       980       985       985       990       990         2837       Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys       2838       995       1000       1005         2839       1010       1000       1005       1005         2840       Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val Asn       1020         2842       1010       1015       1020         2842       1030       1035       1040         2844       1025       1030       1035       1040         2845       1046       Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn       1045       1050       1055         2848       2849       Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly       1065       1070         2851       Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser       1085         <			_		_		_		_	_	_	_	_	_			_
2830 2831			Asp	Ile	Asn	Glu	_	Ala	Ser	Asp	Pro	_	Arg	Asn	Gly	Ala	
Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly Phe 2832   965   970   970   975   975   975   9833   984   Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser 2835   980   985   985   990   985   990   985   990   9836   985   990   985   985   990   990   985   990   985   990   985   990   985   990   985   990   985   990   985   990   985   990   985   990   985   990   990   985   990   985   990   985   990   985   990   985   990   990   985   990		945					950					955					960
2832 965 970 975  2833  2834 Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser 2835 980 985 990  2836  2837 Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys 2838 995 1000 1005  2839  2840 Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val Asn 2841 1010 1015 1020  2842  2843 Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly 2844 1025 1030 1035 1040  2845  2846 Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn 2847 1045 1050 1055  2848  2849 Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly 2850 1060 1065 1070  2851  2852 Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser 2853 1075 1080 1085						_											
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2837					980					985					990		
2838 995 1000 1005 2839 2840 Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val Asn 2841 1010 1015 1020 2842 2843 Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly 2844 1025 1030 1035 1040 2845 2846 Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn 2847 1045 1055 2848 2849 Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly 2850 1060 1065 1070 2851 2852 Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser 2853 1075 1080 1085 2854 2855 Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val	2836																
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Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln Asp Gly 2844  1025  1030  1035  1040  2845  2846  Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn 2847  1045  2848  2849  Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly 2850  1060  2851  2852  Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser 2853  2854  2855  Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val	2841		1010	)				1015	5				1020	)			
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2846 Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr Gly Pro Asn 2847 1045 1050 1055  2848  2849 Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly 2850 1060 1065 1070  2851  2852 Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser 2853 1075 1080 1085  2854  2855 Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val	2844	1025	5				1030	)				1035	5				1040
2847 2848 2849 2849 2850 2851 2852 2852 2853 2854 2855 3075 3085 3085 3085 3085 3085 3085 3085 308	2845																
2848 2849	2846	Arg	Gly	Leu	His	Arg	Cys	Thr	Cys	Pro	Gln	Gly	Tyr	Thr	Gly	${\tt Pro}$	Asn
2849 Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro Cys Lys Asn Gly 2850 1060 1065 1070  2851  2852 Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg Cys Glu Cys Pro Ser 2853 1075 1080 1085  2854  2855 Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val	2847					1045	5				1050	)				1059	5
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2855 Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro Ser Val Ser Cys Glu Val	2853	_		_	_						•	_			_		
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## RAW SEQUENCE LISTING PATENT APPLICATION US/08/083,590

TIME: 13:13:49

DATE: 12/16/93

2857															
2858	Ala Al	a Gln	Ara	Gln	Glv	W=1	λen	Val	λla	ħrα	Len	Cvc	Cln	Ti c	Clv
2859	1105	a Giii	ALG	GIII	111		App	vai	ALG	111!		Cys	GIII	птэ	1120
2860	1103					,					,				1120
2861	Gly Le	n Cve	Val	Δen	Δla	Glv	Δen	Thr	Hic	Hie	Cve	Ara	Cve	Gln	λla
2862	O1, 10	u cyb	var	112!		O <sub>T</sub> y	71011		1130		Cyb	n-9	Cys	1135	
2863					•				110	•				113.	,
2864	Gly Ty	r Thr	Glv	Ser	Tur	Cve	Glu	Agn	T.e.11	Val	λen	Glu	Cvc	Sar	Dro
2865	Oly ly		1140		- y -	Cys	GLU	114		Val	тэр	GIU	1150		FIO
2866			T14,	0					,				113	,	
2867	Ser Pr	o Cre	Cln	λan	Clv.	ת 1 ת	Thr	Cva	Thr	7) cm	Тиг	T 011	C111	C1	The sace
2868	SCI FI	115		ASII	Gry	ALA	1116	_	1111	Азр	ı yı	116	_	Gry	TYL
2869		113.	,				110	J				110.	,		
2870	Ser Cy	e Twe	Care	Val	λla	Gly	Туг	Uic	GI v	Wal	λen	Cvc	Sor	Glu	Glu
2871	_	.70	Cys	Val	Ата	117!	_	птэ	Gry	vai	1180	_	261	Giu	GIU
2872		. 70				11/.	,				110	,			
2873	Ile As	n Clu	Carc	T 011	cor	ui a	Dro	Czza	C15	7 02	C1	C1	The	Crea	T ou
2874	118 AS	p Gru	Cys	пеп	119		PIO	Cys	GIII	119	_	GIY	1111	Cys	1200
2875	1102				113	J				113	,				1200
2876	Asp Le	Dro	7 an	Thr	T172	Tara	Cvc	C02	Crra	Dro	7 200	<b>~1</b>	Thr	C15	C111
2877	ASP LC	u PIO	ASII	120!	_	цуэ	Суъ	Ser	121		ALG	GIY	1111	1215	_
2878				120	,				121	,				1213	,
2879	Val Hi	a Crra	Clu	т1.	7 an	1701	7 an	7 an	Cara	7 an	Dro	Dwo	1707	7 00	Dro
2880	val ni	s Cys	1220		ASII	vai	ASP	122!	_	ASII	PIO	PIO		_	PIO
2881			1221	J				122	•				1230	,	
2882	Val Se	x 7x~	Cox	Dro	T	Crra	Dho	7 ~~	7 ~~	~1	The	Crra	370 J	7 ~~	<i>0</i> 15
2883	var se	123		PIO	пув	Cys			ASII	GIY	1111	-		Asp	GIII
		123	5				1240	J				124	>		
2884	17al 01	01	[[] <sub>2</sub> = 20	C 0.20	<b>C</b>	mb	a	Dece	Droo	a1	Dha	7707	<b>~</b> 1	a1	7
2885 2886	Val Gl	у <u>Сту</u> 50	IYL	ser	Cys	125	_	PIO	PIO	GIY	1260		GTA	GIU	Arg
2887	12	50				123	•				120	J			
2888	Crra Cl		7 000	1707	7 ~~	<i>α</i> 1	C	т о	Cor	7 an	Dwo	C	7 ~~	77.	7 200
2889	Cys Gl 1265	u Giy	ASP	val	1270		Cys	пеп	Ser	127		Cys	Asp	АТА	1280
2890	1205				12/1	J				12/:	)				1200
2891	Gly Th	r Cln	7 cm	Cara	1727	Cl n	7 200	ו בעו	7 an	7 an	Dho	шia	Cva	C111	Cva
2892	GIY II.	.r Giii	ASII	128!		GIII	Arg	vai	1290		PHE	птэ	Cys	1295	
2893				120.	,				1231	J				1295	,
2894	Arg Al	- Cl.	uia	The	C1	7 ~~	7 **	Cara	C1,,	602	1701	т1.	7 an	C1.	Cvc
2895	Arg Ar	a Giy	1300		СТУ	Arg	Arg	130!		Ser	vai	TTE	1310	_	Cys
2896			1300	J				130	-				131	,	
2897	T.v.a. C1	T	Dro	Cva	Tara	7 cn	C1.,	C1.,	Thr	Cara	717	1707	ת ד ת	802	λαn
2898	Lys Gl			Суб	пуъ	ASII			1111	Cys	нта	132		SET	ASII
2899		131	5				1320	J				132	5		
	The Al	2 7 xc	C1.,	Dho	Tlo	CTTC	Tara	Cva	Dro	ת 1 ת	C1.	Dho	G111	C111	מות
2900 2901	Thr Al	a Arg	GTÀ	FIIE	116	133!	_	Cys	FIO	AId	134(		GIU	GIY	ATG
2901	13	30				133:	,				T24/	,			
2902	Thr C	e Cl.	7 c.~	7) cm	7.1 ~	7 ~~	Thr	Circ	ردان معالی	Ser	Lon	7~~	Carc	Len	Λαn
2903 2904	Thr Cy 1345	o GIU	ASII	нар	1350		TIIL	Cys	GTA	135!		мr	Cys	пеи	1360
2904	T3#3				1331	,				133:	,				1300
2906	Gly Gl	ኒ ምክም	Cve	Tle	Ser	<u>61.7</u>	Dro	Δνα	Ser	Dro	Thr	Cve	Leu	Cve	T.eu
2907	GIA GI	A TITE	Cys	136		GIY	F10	AT 9	1370		TILL	Cys	Leu	1375	
2901				<b></b> 0.	,				13/					13/5	,

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2000																
2908 2909	C1.,	Dro	Dho	The	~1	Dro	<b>~1.</b> ,	C1.0	~1 m	Dha	Dwo	77.	C	0	D	C
2910	Gry	PIO	PHE	1380		PIO	GIU	Cys			PIO	Ald	ser		Pro	Cys
2911				130	J				138	5				139	J	
2912	т	<b>a</b> 1	<b>~1</b>	7	D	a	M	7	<b>a</b> 1	<b>a</b> 1	m1	<b>~</b>	<b>~</b> 1	D	m1	
	ьeu	GIA			PIO	Сув	Tyr			GIY	Thr	Cys			Thr	ser
2913			139	5				1400	J				140	5		
2914	<b>G</b> 3	0	D	DI	m	7	<b>~</b>	<b>.</b>	~	D			1	_	~7	_
2915	GIU			Pne	Tyr	Arg	_		Cys	Pro	Ата	_		Asn	Gly	Leu
2916		1410	U				141!	•				1420	U			
2917		~			_	_		_	-1	~-7		~-3		~	_	_
2918			HIS	тте	ьeu			ser	Pne	GTA			Ala	GIY	Arg	
2919	142	<b>5</b>				1430	)				143	5				1440
2920		_	_	_	_					_		_	_			
2921	IIe	Pro	Pro	Pro			GLu	GLu	Ala	_		Leu	Pro	Glu	Cys	
2922					1445	Ō				1450	)				1455	5
2923		_			_						_					
2924	Glu	Asp	Ala			Lys	Val	Cys			Gln	Cys	Asn	Asn	His	Ala
2925				1460	)				146	5				1470	)	
2926																
2927	Cys	Gly	_	_	Gly	Gly	Asp	Cys	Ser	Leu	Asn	Phe	Asn	Asp	Pro	Trp
2928			147	5				1480	)				148	5		
2929																
2930	Lys		_	Thr	${\tt Gln}$	Ser	Leu	Gln	Cys	$\mathtt{Trp}$	Lys	Tyr	Phe	Ser	Asp	Gly
2931		1490	0				1495	5				1500	)			
2932																
2933	His	Cys	Asp	Ser	Gln	Cys	Asn	Ser	Ala	Gly	Cys	Leu	Phe	Asp	Gly	Phe
2934	150	5				1510	)				1515	5				1520
2935																
2936	Asp	Cys	Gln	Arg	Ala	Glu	Gly	${\tt Gln}$	Cys	Asn	Pro	Leu	Tyr	Asp	Gln	Tyr
2937					1525	5				1530	) (				1535	5
2938																
2939	Cys	Lys	Asp	His	Phe	Ser	Asp	Gly	His	Cys	Asp	Gln	Gly	Cys	Asn	Ser
2940				1540	)				154	5				1550	)	
2941																
2942	Ala	Glu	Cys	Glu	Trp	Asp	Gly	Leu	Asp	Cys	Ala	Glu	His	Val	Pro	Glu
2943			155	5				1560	)				156	5		
2944																
2945	Arg	Leu	Ala	Ala	Gly	Thr	Leu	Val	Val	Val	Val	Leu	Met	Pro	Pro	Glu
2946	,	1570	)				1575	5				1580	)			
2947																
2948	Gln	Leu	Arg	Asn	Ser	Ser	Phe	His	Phe	Leu	Arg	Glu	Leu	Ser	Arg	Val
2949	158					1590					159				_	1600
2950																
2951	Leu	His	Thr	Asn	Val	Val	Phe	Lys	Arg	Asp	Ala	His	Gly	Gln	Gln	Met
2952					1605			•	_	1610			-		1615	
2953																
2954	Ile	Phe	Pro	Tyr	Tyr	Gly	Arg	Glu	Glu	Glu	Leu	Arg	Lys	His	Pro	Ile
2955				1620		_	•		1625				-	1630		
2956					-											
2957	Lys	Arg	Ala	Ala	Glu	Gly	Trp	Ala	Ala	Pro	Asp	Ala	Leu	Leu	Gly	Gln
2958	·	=	163			_	_	1640			_		164		-	

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2959															
2960	Val Ly	s Ala	Ser	Leu	Leu	Pro	Glv	Glv	Ser	Glu	Glv	Glv	Δrα	Δra	Δrα
2961	16				200	165	-	O <sub>T</sub> y	561	014	166	-	m g	n-9	n g
2962		-				100.	•				100	,			
2963	Arg Gl	u Leu	Asp	Pro	Met	Asp	Val	Ara	Glv	Ser	Tle	Val	Tyr	Len	Glu
2964	1665				1670		• • •	9		167		· u_	- 7 -	LCu	1680
2965						•					_				1000
2966	Ile As	n Asn	Δrα	Gln	Cvg	Val	Gln	Δla	Ser	Ser	Gln	Cve	Dhe	Gln	Ser
2967	110 110	9 11011	**-9	168	_	V 4 1	0111	nia	169		0111	Cyb	1110	1695	
2968				100.	•				100					10).	,
2969	Ala Th	r Agn	Va 1	Δla	Δla	Dhe	T. <del>0</del> 11	Glv	Δla	T.e.11	Δla	Ser	T.e.u	G1 v	Ser
2970		p	170		1114			170		LCu	2124	501	1710	_	001
2971				•				<b>1</b> ,0.	•				± / ± \	,	
2972	Leu As	n Tle	Pro	Tvr	Lvs	Tle	Glu	Δla	Val	Gln	Ser	Glu	Thr	Val	Glu
2973	1100 110	171		-1-	_,		172		· · · ·	0411	501	172		Vai	Olu
2974			_				± , 2	•				1,2.	•		
2975	Pro Pr	n Dro	Pro	Δla	Gln	T.011	Hic	Dhe	Mot	Туг	Wa l	λla	Δla	Δla	Δla
2976	17		110	ALG	GIII	173		FIIC	1.100	T Y T	1740		лта	лта	AIG
2977	Ι,	30				1,0	,				1/4	,			
2978	Phe Va	1 T.e.11	T.e.11	Dhe	Dhe	Val	Gl v	Cve	G1v	Val	T.611	T.611	Sar	Δνα	Tage
2979	1745	т пец	пси	FIIC	1750		GLY	Cys	Gry	175		пец	SCI	Arg	1760
2980	1/43				1/3	0				1/3	,				1700
2981	Arg Ar	~ 7×~	Gln	шie	Clv	Gln	Len	Trn	Dhe	Dro	Glu	Glv	Dho	Larg	Wa I
2982	ary ar	a vra	GIII	176!	_	GIII	пси	тър	1770		GIU	GLY	FIIC	1775	
2983				170.	,				1//	J				1//-	,
2984	Ser Gl	בות נ	Sar	Larg	Luc	Lare	λrα	Λrα	Glu	Glu	Len	Gl <sub>3</sub>	Glu	λαn	Cor
2985	ser Gr	u Ala	178	_	пуъ	пур	Arg	178		Giu	пеп	GIY	1790	_	ser
2986			1/0	U				1/0:	3				1/50	,	
2987	Val Gl	z T.em	Larg	Dro	T.011	Laze	λcn	777 -	Cor	λcn	Clv	ת 1 ת	LON	Mot	λan
2988	var Gr	у Бей 179		FLO	neu	пуъ	1800		261	Asp	Gry	180		Mec	АБР
2989		115	,				100	J				100.	,		
2990	Asp As	a Gla	λan	Glu	Trn	Gl v	Λen	Glu.	Λαn	T.011	Glu	Thr	Larg	Laze	Dho
2991	18		ASII	GIU	тър	181!	_	GIU	Asp		1820		цуъ	пуъ	FIIC
2992	10	10				101.	,				102	,			
2993	Arg Ph	a G] 11	Glu	Dro	Val	Val	T.611	Dro	λen	T.A11	λen	Aen	Gln	Thr	Agn
2994	1825	e Giu	Giu	FIO	183		шец	FIO	тэр	183	_	тэр	GIII	1111	1840
2995	1025				100	0				105.	,				1040
2996	His Ar	r Gln	Trn	Thr	Gln	Gln	Hie	T. <b>-</b> 11	Δen	<b>Δ</b> ] =	בומ	Agn	T.211	Δνα	Mot
2997	IIIO AL	9 0111	115	184		GIII	1113	шси	1850		AIG	тор	пси	1855	
2998				101.	,				100					105.	,
2999	Ser Al	a Met	7 J =	Dro	Thr	Dro	Dro	Gln	Gl v	Glu	Val	λen	בוג	λen	Cve
3000	OCI AI	a rice	186		1111	110	110	186		OLU	VUL	Hop	1870		Cys
3001			100.	•				100.	,				1070	,	
3002	Met As	o Wal	Aen	V21	Δνα	Glv	Dro	Agn	Glv	Dhe	Thr	Dro	T.A11	Mot	Tla
3002	cc Ab	187		V	9	Ψ±y	1880	_	C + y	1110		188			
3004		207	-				_550	-					-		
3005	Ala Se	r Cve	Ser	G] v	Glv	Glv	Len	Glii	Thr	Glv	Asn	Ser	Glu	Glu	Glu
3006	18	_	201	- <u>'</u>	- Y	189				CLY	1900		ψ± u	u	J_ u
3007		- 0					-					-			
3008	Glu As	o Ala	Pro	Ala	Val	Ile	Ser	Asp	Phe	Ile	Tvr	Gln	Glv	Δla	Ser
3009	1905				1910					191	_	<b>U</b>			1920
						-					_				

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2010																
3010	T	TT4	7	~1	m1	3	3	m1	<b>~1</b>	<b>a</b> 1	m1		<b>.</b>			
3011	Leu	HIS	ASI	GIN			Arg	Thr	GIY			Ата	ьeu	His		
3012					1925	)				193	U				193	•
3013	77-	7		<b>a</b>	7	0	3		27.	<b>.</b>		<b>.</b>	<b>.</b>	<b>a</b> 1		_
3014	Ата	arg	Tyr			ser	Asp	Ата		_	Arg	ьeu	ьeu	Glu		Ser
3015				1940	J				194	5				1950	י	
3016		-		_	~7	<b>~</b> 1				~1	_	1	_	_	1	
3017	Ата	Asp			тте	GIN	Asp			GIY	Arg	Thr		Leu	His	Ala
3018			195	•				196	Ú				196	5		
3019			_		_								_			_
3020	Ala			Ala	Asp	Ala			Val	Phe	GIn			Ile	Arg	Asn
3021		1970	)				197	5				1980	0			
3022	_	_ ~		_	_	_		_			_		•		_	_
3023			Thr	Asp	Leu	_		Arg	Met	His		_	Thr	Thr	Pro	
3024	198	5				1990	)				199	5				2000
3025							_	_		_			_			_
3026	Ile	Leu	Ala	Ala	_		Ala	Val	Glu	_		Leu	Glu	Asp		
3027					2009	5				201	0				2015	5
3028																
3029	Asn	Ser	His			Val	Asn	Ala		_	Asp	Leu	Gly	Lys	Ser	Ala
3030				2020	)				202	5				2030	)	
3031																
3032	Leu	His	Trp	Ala	Ala	Ala	Val	Asn	Asn	Val	Asp	Ala	Ala	Val	Val	Leu
3033			203	5				2040	0				204	5		
3034																
3035	Leu	Lys	Asn	Gly	Ala	Asn	Lys	Asp	Met	Gln	Asn	Asn	Arg	Glu	Glu	Thr
3036		2050	)				205	5				2060	)			
3037																
3038	Pro	Leu	Phe	Leu	Ala	Ala	Arg	Glu	Gly	Ser	Tyr	Glu	Thr	Ala	Lys	Val
3039	2069	5				2070	)				207	5				2080
3040																
3041	Leu	Leu	Asp	His	Phe	Ala	Asn	Arg	Asp	Ile	Thr	Asp	His	Met	Asp	Arg
3042					2085	5				209	0				2095	5
3043																
3044	Leu	Pro	Arg	Asp	Ile	Ala	Gln	Glu	Arg	Met	His	His	Asp	Ile	Val	Arg
3045				2100	)				210	5				2110	)	
3046																
3047	Leu	Leu	Asp	Glu	Tyr	Asn	Leu	Val	Arg	Ser	Pro	Gln	Leu	His	Gly	Ala
3048			211	5				2120	C				212	5		
3049																
3050	Pro	Leu	Gly	Gly	Thr	Pro	Thr	Leu	Ser	Pro	Pro	Leu	Cys	Ser	Pro	Asn
3051		2130	)				213	5				2140	)			
3052																
3053	Gly	Tyr	Leu	Gly	Ser	Leu	Lys	Pro	Gly	Val	Gln	Gly	Lys	Lys	Val	Arg
3054	2145	5		-		2150	)		_		215	5	-	-		2160
3055																
3056	Lys	Pro	Ser	Ser	Lys	Gly	Leu	Ala	Cys	Gly	Ser	Lys	Glu	Ala	Lys	Asp
3057					2165	5				217	)				2175	5
3058																
3059	Leu	Lys	Ala	Arg	Arg	Lys	Lys	Ser	Gln	Asp	Gly	Lys	Gly	Cys	Leu	Leu
3060				2180	)				218	5				2190	)	

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3061																
3062	Δen	Car	Sar	Gly	Mot	T.011	Car	Dro	Val	λen	Cor	Lou	Clu	cor	Dro	Uic
3063	лэр	Jei	219	_	Mec	пси	Ser	2200		Asp	261	пеп	220!		PIO	птъ
3064			21).	,				2201	,				220.	,		
3065	Glv	Tur	T.e.11	Ser	Δan	Val	Δla	Ser	Dro	Dro	T.A11	T.A11	Dro	Sar	Dro	Dhe
3066	017	221		DCI	пор	Val	2215		110	FIO	пец	2220		561	FIO	FIIC
3067		221	•				221.	,				222	,			
3068	Gln	Gln	Ser	Pro	Ser	Va 1	Dro	T.011	λen	Hic	T.011	Dro	Glaz	Mot	Dro	Λαn
3069	222		Der	FIO	Ser	2230		пеп	ASII	птэ	223		Gry	MEC	PIO	2240
3070	222	<b>J</b>				223	J				223.	,				2240
3071	Thr	Hie	T.A11	Gly	Tla	Glv	Hic	T.011	λan	Wa l	λla	ת ות	Larc	Dro	Gl <sub>11</sub>	Mat
3072	1111	mis	пеп	Gry	2245		птъ	ьеu	ASII	2250		AIA	цуѕ	PIO	225	
3072					441.	,				445	,				225	•
3074	בות	Λla	T.011	Gly	Gl v	Gl <sub>37</sub>	Gl v	λνα	LOU	ת 1 ת	Dhe	Glu	Thr	C111	Dro	Dro
3075	лта	ALG	шец	2260	_	GIY	GTÅ	Arg	2265		FILE	GIU	TILL	2270		PIO
3075				2200	,				220	,				22/	,	
3077	λνα	T.011	Car	His	T.011	Dro	T/a l	712	Sar	Gl <sub>37</sub>	Thr	Car	Thr	Val	LOU	Gl <sub>11</sub>
3078	Arg	пец	227		пец	PIO	vai	2280		Gry	1111	ser	228		Leu	GIA
3078			22/:	3				2201	,				220:	5		
3079	Sar	Sar	Sor	Gly	Gl v	בות	Lau	Nan	Dho	Thr	1701	C111	Cly	C02	Thr	cor
3081	Der	229		GLY	Gry	AIA	229		FIIC	1111	vaı	2300	_	Ser	1111	Ser
3082		223	,				223	)				2300	,			
3082	Lou	Λan	Clar	Cln	Cara	Clu	Trn	T 011	cor	7 ~~	T 011	Cl n	602	C1.,	Mo+	val
3084			GIY	Gln	Cys			ьeu	Ser	Arg			ser	GIY	Mec	2320
3085	230	5				2310	,				2319	•				2320
3086	Dro	7 an	Cln	Т122	7 00	Dro	T 011	7 ~~~	C1	Com	1707	71.	Dwo	<b>~1</b>	Dwo	T 011
3087	PIO	ASII	GIII	Tyr	2325		Бец	Arg	GTA	2330		мта	PIO	GIY	2335	
3088					232:	,				233(	,				233	,
3089	cor	Thr	Cln.	Ala	Dro	202	T 011	Cln	uic	C111	Mo+	3707	C1.	Dxo	T 011	uia
3090	Ser	1111	GIII	2340		261	пец	GIII	2345		MEC	vai	GLY	2350		птъ
3091				2340	,				2343	)				2350	,	
3092	Sor	Ser	T.011	Ala	λla	Car	ת דת	Lou	Car	Cln.	Mot	Mot	202	Тиг	Gln.	Gl <sub>11</sub>
3093	ber	Jei	235		AIG	Der	Ата	2360		GIII	1-10-0	Mec	236	_	GIII	Gry
3094			233.	,				2500	,				250.	,		
3095	Len	Pro	Ser	Thr	Δrα	T.em	Δla	Thr	Gln	Pro	His	T.e11	Val	Gln	Thr	Gln
3096	Leu	237		1111	y	шец	2375		0111	110	****	2380		GIII	1111	0111
3097												2500	•			
3098	Gln	Val	Gln	Pro	Gln	Asn	Leu	Gln	Met	Gln	Gln	Gln	Asn	Len	Gln	Pro
3099	238		<b></b>			2390		02		<b></b>	239			LCu	<b></b>	2400
3100							-					•				
3101	Ala	Asn	Ile	Gln	Gln	Gln	Gln	Ser	Leu	Gln	Pro	Pro	Pro	Pro	Pro	Pro
3102					2405					2410					2419	
3103						-					_					
3104	Gln	Pro	His	Leu	Glv	Val	Ser	Ser	Ala	Ala	Ser	Glv	His	Leu	Glv	Ara
3105				2420					2425			4		2430	_	
3106														'		
3107	Ser	Phe	Leu	Ser	Glv	Glu	Pro	Ser	Gln	Ala	Asp	Val	Gln	Pro	Leu	Glv
3108	_		243		4	-	-	2440		• •	- T-	•	2445			4
3109																
3110	Pro	Ser	Ser	Leu	Ala	Val	His	Thr	Ile	Leu	Pro	Gln	Glu	Ser	Pro	Ala
3111		245					245					2460				

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3112		
3113	Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro Pro Val Thr Ala Ala	
3114	2465 2470 2475 2480	
3115		
3116	Gln Phe Leu Thr Pro Pro Ser Gln His Ser Tyr Ser Ser Pro Val Glu	
3117	2485 2490 2495	
3118		
3119	Asn Thr Pro Ser His Gln Leu Gln Val Pro Glu His Pro Phe Leu Thr	
3120	2500 2505 2510	
3121		
3122	Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Pro His Ser	
3123	2515 2520 2525	
3124		
3125	Asn Val Ser Asp Trp Ser Glu Gly Val Ser Ser Pro Pro Thr Ser Met	
3126	2530 2535 2540	
3127		
3128	Gln Ser Gln Ile Ala Arg Ile Pro Glu Ala Phe Lys	
3129	2545 2550 2555	
3130		
3131	(2) INFORMATION FOR SEQ ID NO:21:	
3132		
3133	(i) SEQUENCE CHARACTERISTICS:	
3134	(A) LENGTH: 9723 base pairs	
3135	(B) TYPE: nucleic acid	
3136	(C) STRANDEDNESS: double	
3137	(D) TOPOLOGY: unknown	
3138		
3139	(ii) MOLECULE TYPE: cDNA	
3140		
3141		
3142	(ix) FEATURE:	
3143	(A) NAME/KEY: CDS	
3144	(B) LOCATION: 107419	
3145		
3146		
3147	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
3148		
3149	GGAATTCCG CCC GCC CTG CGC CCC GCT CTG CTG TGG GCG CTG CT	3
3150	Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala	
3151	1 5 10	
3152		
3153	CTC TGG CTG TGC TGC GCG GCC CCC GCG CAT GCA TTG CAG TGT CGA GAT	5
3154	Leu Trp Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp	
3155	15 20 25	
3156		
3157	GGC TAT GAA CCC TGT GTA AAT GAA GGA ATG TGT GTT ACC TAC CAC AAT	4
3158	Gly Tyr Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn	
3159	30 35 40 45	
3160	,	
3161	GGC ACA GGA TAC TGC AAA TGT CCA GAA GGC TTC TTG GGG GAA TAT TGT	2
3162	Gly Thr Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys	

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3163					50					55					60		
3164 3165	CDD	CAT	CGA	GAC	ccc	ጥርም	GNG	אאכ	አአሮ	cac	тас	CNG	ייי א א	CCT	ccc	አርጥ	240
3166	_	His															240
3167			5	65		-1-		-1 -	70	5	-1-			75	1		
3168																	
3169		GTG															288
3170	Cys	Val		Gln	Ala	Met	Leu		Lys	Ala	Thr	Cys		Cys	Ala	Ser	
3171			80					85					90				
3172	aaa	mmm	7 (7	aa 2	a 2 a	a 2 a	maa	<b>a</b> a	ma c	max.	7 (7 7	mam	C A C	007	шаа	mmm	226
3173 3174		TTT Phe															336
3175	Gry	95	1111	СТУ	GIU	Asp	100	GIII	TYL	Ser	1111	105	птъ	PIO	Cys	PILE	
3176		,,,					100					100					
3177	GTG	TCT	CGA	CCC	TGC	CTG	AAT	GGC	GGC	ACA	TGC	CAT	ATG	CTC	AGC	CGG	384
3178		Ser															
3179	110		_		-	115		_	_		120					125	
3180																	
3181	GAT	ACC	TAT	GAG	TGC	ACC	TGT	CAA	GTC	GGG	TTT	ACA	GGT	AAG	GAG	TGC	432
3182	Asp	Thr	Tyr	Glu	Cys	Thr	Cys	Gln	Val	Gly	Phe	Thr	Gly	Lys	Glu	Cys	
3183					130					135					140		
3184																	
3185		TGG															480
3186	GIN	Trp	Thr	_	Ата	Cys	ьeu	ser		Pro	Cys	Ата	ASN	_	ser	Thr	
3187 3188				145					150					155			
3189	тст	ACC	ΔСТ	стс	פככ	ממכ	CAG	ጥጥር	TCC	TGC	ΔΔΔ	TGC	СТС	מט	GGC	ጥጥር	528
3190		Thr															320
3191	C <sub>I</sub> S		160	V W Z			0111	165		Cys	,	Cys	170	****	<b>-</b> 1	1110	
3192																	
3193	ACA	GGG	CAG	AAA	TGT	GAG	ACT	GAT	GTC	AAT	GAG	TGT	GAC	ATT	CCA	GGA	576
3194	Thr	Gly	Gln	Lys	Cys	Glu	Thr	Asp	Val	Asn	Glu	Cys	Asp	Ile	Pro	Gly	
3195		175					180					185					
3196																	
3197		TGC															624
3198		Cys	Gln	His	GLY	_	Thr	Cys	Leu	Asn		Pro	GLY	Ser	Tyr		•
3199	190					195					200					205	
3200 3201	TCC	CAG	TCC	CCT	מאפ	ccc	ጥጥር	אכא	ccc	CAG	ጥአሮ	ጥርም	GAC	አርሮ	СТС	ጥለጥ	672
3202		Gln															072
3203	Cys	GIII	СуБ	FIO	210	Gry	FIIC	1111	GLY	215	ı yı	Cys	АЗР	DCI	220	- y -	
3204																	
3205	GTG	CCC	TGT	GCA	CCC	TCA	CCT	TGT	GTC	AAT	GGA	GGC	ACC	TGT	CGG	CAG	720
3206		Pro															
3207			_	225				-	230		-	-		235	_		
3208																	
3209		GGT															768
3210	Thr	Gly	_	Phe	Thr	Phe	Glu	_	Asn	Cys	Leu	Pro	_	Phe	Glu	Gly	
3211			240					245					250				
3212	700	ממ	man.	C7.C	אממ	አ አ <del>ጠ</del>	א נחנה	C A m	C7 C	таа	ccm	7 7 C	C 7 C	700	m/cm	CZC	016
3213	AGC	ACC	IGI	GAG	AGG	AAT	ATT	GAT	GAC	TGC	CCT	AAC	CAC	AGG	IGT	CAG	816

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3214 3215 3216	Ser	Thr 255	Cys	Glu	Arg	Asn	Ile 260	Asp	Asp	Cys	Pro	Asn 265	His	Arg	Cys	Gln	
3217 3218 3219 3220				GTT Val													864
3221 3222 3223 3224				TGG Trp													912
3225 3226 3227 3228				CCC Pro 305			-	_									960
3229 3230 3231 3232				TAT Tyr													1008
3233 3234 3235 3236				AAC Asn													1056
3237 3238 3239 3240				ATC Ile													1104
3241 3242 3243 3244				GGT Gly													1152
3245 3246 3247 3248				AAG Lys 385													1200
3249 3250 3251 3252				ACC Thr													1248
3253 3254 3255 3256	_		_	GAA Glu				_								_	1296
3257 3258 3259 3260				GTG Val													1344
3261 3262 3263 3264				GGA Gly													1392

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3265 3266 3267 3268		TGC Cys							1440
3269 3270 3271 3272		CTG Leu 480							1488
3273 3274 3275 3276		GAA Glu							1536
3277 3278 3279 3280		GTC Val							1584
3281 3282 3283 3284		TGC Cys							1632
3285 3286 3287 3288		GCA Ala							1680
3289 3290 3291 3292		GGT Gly 560							1728
3293 3294 3295 3296		GAT Asp							1776
3297 3298 3299 3300		TGC Cys							1824
3301 3302 3303 3304		GAT Asp							1872
3305 3306 3307 3308		CTG Leu							1920
3309 3310 3311 3312		AAT Asn 640							1968
3312 3313 3314 3315		GGA Gly							2016

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DATE: 12/16/93 TIME: 13:14:51

3316	max.	CCA	CC 3	mma	7 (7)	aaa	a 2 a	707	mam	770	2 000	an a	2 000	C A III	a	mam	2064
3317 3318														GAT			2064
3319	670	PIO	GIY	Pne	1111	675	GIII	Arg	Cys	ASII		Asp	TTE	Asp	GIU	_	
3320	670					0/5					680					685	
3321	CCC	Tr.C.C	א א תי	aaa	m/cm	aaa	777	CCT	aan	7 (7	m/cm	7 mc	770	GGT	СТС	7 7 177	2112
3321																	2112
3322	нта	261	ASII	PIO	690	Arg	пур	GIY	Ата	695	Cys	TTE	ASII	Gly		ASII	
3324					030					093					700		
3325	CCT	ጥጥር	CGC	тcт	אידיא	TCC	מממ	GNG	CCA	ccc	СУП	CAC	ccc	AGC	TCC	ጥልሮ	2160
3326														Ser			2100
3327	Gry	1110	A. 9	705	110	Cys	110	Olu	710	110	1113	1113	110	715	Cys	TYT	
3328				, 05					, 10					, 13			
3329	TCA	CAG	GTG	AAC	GAA	TGC	СТС	AGC	דעע	כככ	TGC	ΔΤС	САТ	GGA	אאכ	тст	2208
3330														Gly			2200
3331			720			-1-		725			07.0		730	<b>-</b> 1		0,70	
3332																	
3333	ACT	GGA	GGT	CTC	AGT	GGA	TAT	AAG	TGT	CTC	TGT	GAT	GCA	GGC	TGG	GTT	2256
3334														Gly			
3335		735	•			•	740	•	-		-	745		•	•		
3336																	
3337	GGC	ATC	AAC	TGT	GAA	GTG	GAC	AAA	AAT	GAA	TGC	CTT	TCG	AAT	CCA	TGC	2304
3338	Gly	Ile	Asn	Cys	Glu	Val	Asp	Lys	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	
3339	750					755	•				760					765	
3340																	
3341	CAG	AAT	GGA	GGA	ACT	TGT	GAC	AAT	CTG	GTG	AAT	GGA	TAC	AGG	TGT	ACT	2352
3342	Gln	Asn	Gly	Gly		Cys	Asp	Asn	Leu	Val	Asn	Gly	Tyr	Arg	Cys	Thr	
3343					770					775					780		
3344																	
3345														ATT			2400
3346	Cys	Lys	Lys		Phe	Lys	GLY	Tyr		Cys	Gln	Val	Asn	Ile	Asp	Glu	
3347				785					790					795			
3348	mam	000	шал	7 7 M	<b>aa</b> 7	шаа	аша	770	C1 7 7	<b>aa</b> 3	7.00	шаа	mmm	a n m	a	7 (11.2)	2440
3349														GAT			2448
3350 3351	Cys	Ата	800	ASII	PIO	Cys	ьeu	805	GIII	Gry	TILL	Cys	810	Asp	Asp	116	
3352			800					805					910				
3353	ΔCT	GGC	ጥልሮ	ΔСТ	тсс	CAC	тст	стс	СТС	CCA	ጥልሮ	מרמ	GGC	AAG	דע ע	тст	2496
3354														Lys			2470
3355	501	815	-1-		O <sub>I</sub> D		820				-1-	825	<b>U</b> _1			C	
3356																	
3357	CAG	ACA	GTA	TTG	GCT	CCC	TGT	TCC	CCA	AAC	CCT	TGT	GAG	AAT	GCT	GCT	2544
3358														Asn			
3359	830					835	-				840	-				845	
3360																	
3361	GTT	TGC	AAA	GAG	TCA	CCA	AAT	TTT	GAG	AGT	TAT	ACT	TGC	TTG	TGT	GCT	2592
3362	Val	Cys	Lys	Glu	Ser	Pro	Asn	Phe	Glu	Ser	Tyr	Thr	Cys	Leu	Cys	Ala	
3363					850					855					860		
3364																	
3365														GAG			2640
3366	Pro	Gly	Trp	Gln	Gly	Gln	Arg	Cys	Thr	Ile	Asp	Ile	Asp	Glu	Cys	Ile	

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3367				865					870					875			
3368																	
3369		AAG															2688
3370	Ser	Lys		Cys	Met	Asn	His	_	Leu	Cys	His	Asn		Gln	Gly	Ser	
3371			880					885					890				
3372																	
3373		ATG															2736
3374	Tyr	Met	Cys	Glu	Cys	Pro	Pro	Gly	Phe	Ser	Gly	Met	Asp	Cys	Glu	Glu	
3375		895					900					905					
3376																	
3377		ATT															2784
3378	Asp	Ile	Asp	Asp	Cys	Leu	Ala	Asn	Pro	Cys	Gln	Asn	Gly	Gly	Ser	Cys	
3379	910					915					920					925	
3380																	
3381		GAT															2832
3382	Met	Asp	Gly	Val	Asn	Thr	Phe	Ser	Cys	Leu	Cys	Leu	Pro	Gly	Phe	Thr	
3383					930					935					940		
3384																	
3385	GGG	GAT	AAG	TGC	CAG	ACA	GAC	ATG	AAT	GAG	TGT	CTG	AGT	GAA	CCC	TGT	2880
3386	Gly	Asp	Lys	Cys	Gln	Thr	Asp	Met	Asn	Glu	Cys	Leu	Ser	$\operatorname{Glu}$	Pro	Cys	
3387				945					950					955			
3388																	
3389	AAG	AAT	GGA	GGG	ACC	TGC	TCT	GAC	TAC	GTC	AAC	AGT	TAC	ACT	TGC	AAG	2928
3390	Lys	Asn	Gly	Gly	Thr	Cys	Ser	Asp	Tyr	Val	Asn	Ser	Tyr	Thr	Cys	Lys	
3391	_		960	_		-		965	-				970		•	-	
3392																	
3393	TGC	CAG	GCA	GGA	TTT	GAT	GGA	GTC	CAT	TGT	GAG	AAC	AAC	ATC	AAT	GAG	2976
3394	Cys	Gln	Ala	Gly	Phe	Asp	Gly	Val	His	Cys	Glu	Asn	Asn	Ile	Asn	Glu	
3395	-	975		-		-	980			•		985					
3396																	
3397	TGC	ACT	GAG	AGC	TCC	TGT	TTC	AAT	GGT	GGC	ACA	TGT	GTT	GAT	GGG	ATT	3024
3398	Cys	Thr	Glu	Ser	Ser	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Val	Asp	Gly	Ile	
3399	990					995			-	-	1000	-		_	-	1005	
3400																	
3401	AAC	TCC	TTC	TCT	TGC	TTG	TGC	CCT	GTG	GGT	TTC	ACT	GGA	TCC	TTC	TGC	3072
3402	Asn	Ser	Phe	Ser	Cys	Leu	Cys	Pro	Val	Gly	Phe	Thr	Gly	Ser	Phe	Cys	
3403					1010		•			101!			-		1020	_	
3404																	
3405	CTC	CAT	GAG	ATC	AAT	GAA	TGC	AGC	TCT	CAT	CCA	TGC	CTG	AAT	GAG	GGA	3120
3406	Leu	His	Glu	Ile	Asn	Glu	Cys	Ser	Ser	His	Pro	Cys	Leu	Asn	Glu	Gly	
3407				1029			_		1030	_		•		1039	_	•	
3408																	
3409	ACG	TGT	GTT	GAT	GGC	CTG	GGT	ACC	TAC	CGC	TGC	AGC	TGC	CCC	CTG	GGC	3168
3410		Cys															
3411		- 1 -	1040	_	1		2	1045	_		- 2 -		1050			4	
3412																	
3413	TAC	ACT	GGG	AAA	AAC	TGT	CAG	ACC	CTG	GTG	AAT	CTC	TGC	AGT	CGG	TCT	3216
3414		Thr															
3415	- 1 -	105		_1 -		-1-	1060					106	_			. = =	
3416																	
3417	CCA	TGT	AAA	AAC	AAA	GGT	ACT	TGT	GTT	CAG	AAA	AAA	GCA	GAG	TCC	CAG	3264

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3418	Pro C	Cys	Lys	Asn	Lys	_		Cys	Val	Gln	-	-	Ala	Glu	Ser		
3419 3420	1070					1075	•				1080	J				1085	
3421	TGC C	מידיר	тст	CCA	тст	GGA	таа	GCT	сст	GCC	тдт	тст	GAC	GTG	CCC	ידעע	3312
3422	Cys I																3312
3423	-7		-1-		1090	_			1	1099	_	<i>- 1</i>	· · · · ·		1100		
3424											-				,		
3425	GTC I	CT	TGT	GAC	ATA	GCA	GCC	TCC	AGG	AGA	GGT	GTG	CTT	GTT	GAA	CAC	3360
3426	Val S	Ser	Cys	Asp	Ile	Ala	Ala	Ser	Arg	Arg	Gly	Val	Leu	Val	Glu	His	
3427				1105	5				1110	)				1115	5		
3428																	
3429	TTG 1																3408
3430	Leu C	Cys			Ser	Gly	Val	_		Asn	Ala	Gly			His	Tyr	
3431			1120	)				1125	5				1130	)			
3432	mam a	77.0	maa	aaa	ama	aaa	m 3 m	3 CI	999	7.00	ma a	mam		a	<b>~~</b> ~	ama	2456
3433	TGT C																3456
3434 3435	Cys C	5111 L135	_	PIO	пеп	GIY	114(		СТУ	ser	IYL	1145		GIU	GIII	Leu	
3436		1133	,				TT#/	,				1143	,				
3437	GAT G	DAF	тст	GCG	דככ	AAC	CCC	ፐርር	CAG	CAC	GGG	GCA	ACA	TGC	АСТ	GAC	3504
3438	Asp G																5501
3439	1150		-1-			1155		-1-			1160			-1-		1165	
3440																	
3441	TTC F	${ m TT} P$	GGT	GGA	TAC	AGA	TGC	GAG	TGT	GTC	CCA	GGC	TAT	CAG	GGT	GTC	3552
3442	Phe I	Ile	Gly	Gly	Tyr	Arg	Cys	Glu	Cys	Val	Pro	Gly	Tyr	Gln	Gly	Val	
3443					1170	)				1175	5				1180	כ	
3444																	
3445	AAC 1																3600
3446	Asn C	Cys	Glu	_		Val	Asp	Glu	_		Asn	Gln	Pro	_		Asn	
3447				1185	5				1190	)				1199	5		
3448 3449	GGA G	700	7.00	m/cm	א נוויים ע	CNC	COTO	CTC	770	CAT	TTTC	אאכ	TOO	TOT.	TOO	CCA	3648
3450	Gly																3040
3451	GIY C	3 ± Y	1200	_	116	тър	пец	1209		111.5	rne	цуз	1210		СуБ	110	
3452				•					•					•			
3453	CCA G	GC	ACT	CGG	GGC	CTA	CTC	TGT	GAA	GAG	AAC	ATT	GAT	GAC	TGT	GCC	3696
3454	Pro G	3ly	Thr	Arg	Gly	Leu	Leu	Cys	Glu	Glu	Asn	Ile	Asp	Asp	Cys	Ala	
3455	1	1215	5	_	_		1220	o -				1225	5 -	_	-		
3456																	
3457	CGG G																3744
3458	Arg G	Зlу	Pro	His	Cys	Leu	Asn	Gly	Gly	Gln	Cys	Met	Asp	Arg	Ile	Gly	
3459	1230					1235	5				1240	כ				1245	
3460																	
3461	GGC T																3792
3462	Gly 7	ryr	ser	Cys	_	_	ьeu	Pro	GTA			GTA	GLU	Arg	_		
3463 3464					1250	J				125	)				1260	J	
3464 3465	GGA G	מב	ΔΤΟ	ממכ	GAG	тсс	כידיכי	TCC	מממ	כככ	TGC	AGC	ጥርጥ	GAG	GGC	AGC	3840
3466	Gly A																2040
3467	C-y F			1265		~ <i>y</i> 5			1270		~ <i>y</i> .5			1279	_		
3468																	

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3469										_		_		TGC			3888
3470	Leu	Asp			Gln	Leu	Thr	Asn	Asp	Tyr	Leu	Cys	Val	Cys	Arg	Ser	
3471			1280	)				128	5				1290	0			
3472																	
3473														TGT			3936
3474	Ala			Gly	Arg	His	_		Thr	Phe	Val	Asp	Val	Cys	Pro	Gln	
3475		129	5				1300	)				130	5				
3476																	
3477														AAC			3984
3478			Cys	Leu	Asn			Thr	Cys	Ala			Ser	Asn	Met		
3479	1310	)				1315	5				1320	כ				1325	
3480																	
3481														GCA			4032
3482	Asp	Gly	Phe	Ile	_	_	Cys	Pro	Pro	-		Ser	Gly	Ala	_	-	
3483					1330	)				1335	5				1340	)	
3484																	
3485														CAG			4080
3486	Gln	Ser	Ser			Gln	Val	Lys			Lys	Gly	Glu	Gln		Val	
3487				1349	5				1350	)				1355	5		
3488																	
3489														CGG			4128
3490	His	Thr			GLY	Pro	Arg	_		Cys	Pro	Ser		Arg	Asp	Cys	
3491			1360	)				1365	•				1370	)			
3492	~-~		~~~		~~~		- ~ ~	~~~		~~ ~	~-~	~~~	~~~			~-~	
3493				_										AGC			4176
3494	GIu		_	Cys	Ala	Ser			Cys	GIn	Hıs	_	_	Ser	Cys	His	
3495		1379	•				1380	)				138	)				
3496	aam	~~~	~~~	~~~	~~	~~	m. m	m	maa	<b></b>	~~ ~		~~~	~~~	~~~		
3497														CCA			4224
3498			Arg	GIn	Pro		-	Tyr	ser	Cys		-	Ата	Pro	Pro		
3499	1390	)				1399	)				1400	)				1405	
3500 3501	шаа	aam	700	000	mam	CI 7 7	ama	ma a	7.00	COR	aaa	000	300	7.00	aam	aam	4070
														ACC			4272
3502	ser	GIA	ser	Arg	_		ьeu	TYL	THE			Pro	ser	Thr			
3503 3504					1410	,				1415	)				1420	,	
3504	aaa	אממ	TO T	CTC	אככ	CAC	ייי אייי	THE THE	ccc	CAC	7. 7. 7.	CCT	aaa	CATE	ccc	CTC	4220
														GAT			4320
3506 3507	Ala	IIII	Cys			GIII	TYL	Cys		_	гÀг	ALA	Arg	Asp 1435	_	vai	
3507				142	,				1430	,				143	)		
3509	TOT	CAT	CAC	ccc	TCC	አአሮ	אממ	сът	acc	TCC	CAG	TCC	CAT	GGG	CCT	CAC	4368
3510														Gly			4366
3510	Cys	Asp	1440		Cys	HOII	261	1445		Cys	GTII	rrb	1450	_	GTÅ	voħ	
3511			T-1-11	,				144	•				T-1-0(				
3512	ጥርነጥ	ጥርጥ	רידירי	ACC	ΔͲሮ	GAG	ממכ	רכר	ፐርር	GCC	מממ	тсс	יייכיר	TCC	CCD	СТТ	4416
3513														Ser			4410
3514	~ J D	1455		****		JIU	1460				11011	146		501		_cu	
3516		_ · · J .	•				_100	-				_ 10.	-				
3517	CCC	TGC	TGG	GAT	TAT	ATC	AAC	AAC	CAG	TGT	GAT	GAG	CTG	TGC	AAC	ACG	4464
3518														Cys			
3519	1470	_	- E	- 1-		1475				- 2 -	1480			4		1485	
																· =	

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3520																	
3521														AGC			4512
3522	Val	GIu	Cys	Leu		_	Asn	Phe	Glu	_		GLY	Asn	Ser	-		
3523					149	)				149	5				1500	)	
3524																	
3525														AAC			4560
3526	Cys	Lys	Tyr	_	_	Tyr	Cys	Ala	Asp	His	Phe	Lys	Asp	Asn	His	Сув	
3527				150	5				1510	)				1515	5		
3528																	
3529	AAC	CAG	GGG	TGC	AAC	AGT	GAG	GAG	TGT	GGT	TGG	GAT	GGG	CTG	GAC	TGT	4608
3530	Asn	Gln	Gly	Cys	Asn	Ser	Glu	Glu	Cys	Gly	Trp	Asp	Gly	Leu	Asp	Cys	
3531			1520	0				152	5				1530	)			
3532																	
3533	GCT	GCT	GAC	CAA	CCT	GAG	AAC	CTG	GCA	GAA	GGT	ACC	CTG	GTT	ATT	GTG	4656
3534	Ala	Ala	Asp	Gln	Pro	Glu	Asn	Leu	Ala	Glu	Gly	Thr	Leu	Val	Ile	Val	
3535		153	5				1540	0				154	5				
3536																	
3537	GTA	TTG	ATG	CCA	CCT	GAA	CAA	CTG	CTC	CAG	GAT	GCT	CGC	AGC	TTC	TTG	4704
3538	Val	Leu	Met	Pro	Pro	Glu	Gln	Leu	Leu	Gln	Asp	Ala	Arg	Ser	Phe	Leu	
3539	1550	0				1555	5				1560	)	_			1565	
3540																	
3541	CGG	GCA	CTG	GGT	ACC	CTG	CTC	CAC	ACC	AAC	CTG	CGC	ATT	AAG	CGG	GAC	4752
3542	Arg	Ala	Leu	Gly	Thr	Leu	Leu	His	Thr	Asn	Leu	Arg	Ile	Lys	Arg	Asp	
3543	_			_	157					1579		_		-	1580	_	
3544																	
3545	TCC	CAG	GGG	GAA	CTC	ATG	GTG	TAC	CCC	TAT	TAT	GGT	GAG	AAG	TCA	GCT	4800
3546														Lys			
3547			1	158				- 2	1590	_	-1-	2		1599			
3548					_					•							
3549	GCT	ATG	AAG	AAA	CAG	AGG	ATG	ACA	CGC	AGA	TCC	CTT	CCT	GGT	GAA	CAA	4848
3550														Gly			1010
3551			1600	_		3		160	_	9			1610	_		<b></b>	
3552				_													
3553	GAA	CAG	GAG	GTG	GCT	GGC	тст	ΔΔΔ	GTC	ттт	СТС	GAA	ΔΤΤ	GAC	AAC	CGC	4896
3554														Asp			1070
3555	GIG	161		Val	niu	OLY	1620	_	Val	1110	пси	162		тор	ADII	S	
3556		101.	•				102	•				102.	•				
3557	CAG	тст	CTT	$C\Delta\Delta$	GAC	тсъ	GAC	CAC	TGC	ጥጥር	ΔAG	ממכ	ACG	GAT	GCA	GCA	4944
3558														Asp			1711
3559	1630	_	val	01	p	163	_	******	Cys	1110	1640			тыр	71 <u>1</u> u	1645	
3560	105	<b>J</b>				105.	,				101	,				1045	
3561	CCA	CCT	СТС	СТС	acc	ጥሮጥ	כאכ	acc	מידימ	CAG	aaa	אככ	СТС	TCA	TAC	CCT	4992
3562														Ser			4992
3563	TTG	TTG	⊥∈u	ц <del>с</del> ц	1650		1112	ATA	116	1659	-	1111	ьeu	DET	1660		
3564					T02	,				100:	,				100	,	
3565	COTO	CITIC	Tr.Cur	CTTC	ama	y Can	מתבי	TCC	CTC	א כיתי	CCA	(L) V	ccc	л Ст	CAC	CTC	5040
3565 3566														ACT			5040
3566 3567	ьeu	val	DGT.	166		DET	GIU	Det	1670		FIO	GIU	₩ī	Thr 1679		Ten	
				T00	ی				TO \(	J				TO /:	,		
3568	CITIC	Tr A Tr	СШС	Cmm	CCT	Стт	CCTT	Cmm	CITIC	אשמ	7 000	CITIC	mmm.	7 000	y mm	CTC	EARR
3569														ATT			5088
3570	ьeu	ıyr	ьeu	ьeu	ата	vaı	ата	vaı	val	тте	тте	ьeu	rue	Ile	тте	neu	

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3571			1680	0				1689	5				1690	)			
3572																	
3573						GCA											5136
3574	Leu	Gly	Val	Ile	Met	Ala	Lys	Arg	Lys	Arg	Lys	His	Gly	Ser	Leu	Trp	
3575		1699	5				1700	)				170	5				
3576																	
3577	CTG	CCT	GAA	GGT	TTC	ACT	CTT	CGC	CGA	GAT	GCA	AGC	AAT	CAC	AAG	CGT	5184
3578	Leu	Pro	Glu	Gly	Phe	Thr	Leu	Arg	Arg	Asp	Ala	Ser	Asn	His	Lys	Arg	
3579	1710	)		_		1719	5	_	_	_	1720	)			_	1725	
3580																	
3581	CGT	GAG	CCA	GTG	GGA	CAG	GAT	GCT	GTG	GGG	CTG	AAA	AAT	CTC	TCA	GTG	5232
3582						Gln											
3583					1730					173		2			1740		
3584						_					_						
3585	CDD	GTC	тсъ	GAA	ССТ	AAC	СТД	בידים	сст	Σ כיπי	GGA	ΔCΔ	ልርጥ	GDD	CAC	таа	5280
3586						Asn											3200
3587	OIII	Val	501	174!		11011	LIC U		1750		Cry	****	DCI	175		119	
3588				1/4.	,				1/5	,				1/3.	,		
3589	CTC	CAT	CAT	C 7 7	ccc	CCC	CAC	CCA	מממ	7 7 7	CITIA	770	CCT	C 7 7	CAT	CAC	5328
3590																	5326
	val	Asp	-		GIY	Pro	GIII		-	ьуѕ	vaı	пÀр			Asp	Giu	
3591			1760	J				1769	•				1770	J			
3592	999		ama	ma.	G. D. D.	<b>GD D</b>	C 7 E	a. a	999		G 3 FF	GG 3	GGG	007	maa	202	E256
3593						GAA											5376
3594	Ата			ser	GIU	Glu	_	_	Pro	тте	Asp	_	_	Pro	Trp	Thr	
3595		1775	>				1780	J				178	>				
3596																	
3597						GCT											5424
3598			His	Leu	Glu	Ala		Asp	Ile	Arg	_		Pro	Ser	Leu		
3599	1790	כ				1799	5				1800	כ				1805	
3600																	
3601						GCA											5472
3602	Leu	Thr	Pro	Pro	Gln	Ala	Glu	Gln	Glu	Val	Asp	Val	Leu	Asp	Val	Asn	
3603					1810	)				181	5				1820	)	
3604																	
3605	GTC	CGT	GGC	CCA	GAT	GGC	TGC	ACC	CCA	TTG	ATG	TTG	GCT	TCT	CTC	CGA	5520
3606	Val	Arg	Gly	Pro	Asp	Gly	Cys	Thr	Pro	Leu	Met	Leu	Ala	Ser	Leu	Arg	
3607				182	5				1830	)				183	5		
3608																	
3609	GGA	GGC	AGC	TCA	GAT	TTG	AGT	GAT	GAA	GAT	GAA	GAT	GCA	GAG	GAC	TCT	5568
3610	Gly	Gly	Ser	Ser	Asp	Leu	Ser	Asp	Glu	Asp	Glu	Asp	Ala	Glu	Asp	Ser	
3611	-	-	1840		-			184		-		_	1850		_		
3612																	
3613	TCT	GCT	AAC	ATC	ATC	ACA	GAC	TTG	GTC	TAC	CAG	GGT	GCC	AGC	CTC	CAG	5616
3614						Thr											
3615		185					1860			- <b>1</b> -		186				. —	
3616																	
3617	GCC	CAG	ACA	GAC	CGG	ACT	GGT	GAG	ДΤС	GCC	СТС	CAC	СТТ	GCA	GCC	CGC	5664
3618						Thr											
3619	1870				3	1875	_	u			1880					1885	
3620	_5,\	-					-				_55	-					
3621	TAC	тсъ	CGG	GCT	GAT	GCT	GCC	AAG	ССТ	СТС	СТС	САТ	GCA	GGT	GCA	GAT	5712
J											010	<u></u>	1				J. 12

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3622 3623 3624	Tyr Ser	Arg Ala	Asp Ala 1890	Ala Ly	ys Arg	Leu Leu 1895	Asp Ala	Gly Ala 190		
3625 3626 3627 3628			GAC AAC Asp Asn 5			Cys Pro				50
3629 3630 3631 3632			CAA GGT Gln Gly	Val P				Asn Arg		)8
3633 3634 3635 3636		Leu Asp	GCC AGG Ala Arg							56
3637 3638 3639 3640			GCT GTG Ala Val 195	Glu G			Glu Leu			)4
3641 3642 3643 3644			AAT GCA Asn Ala 1970						His	52
3645 3646 3647 3648			GTC AAT Val Asn 5			Ala Thr				00
3649 3650 3651 3652			CGA GAC Arg Asp	Met G				Thr Pro		18
3653 3654 3655 3656		Ala Ala	CGG GAG Arg Glu							96
3657 3658 3659 3660			AAT CGA Asn Arg 203	Asp I			Met Asp			14
3661 3662 3663 3664			CGG GAT Arg Asp 2050						Leu	€2
3665 3666 3667 3668			GTG ACC Val Thr 5			Pro Gly				10
3669 3670 3671 3672			GTC ATC Val Ile	Cys G		-		Leu Ser		38

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3673	AAG	CAC	ACC	CCA	ATG	GGC	AAG	AAG	TCT	AGA	CGG	CCC	AGT	GCC	AAG	AGT	6336
3674	Lys	His	Thr	Pro	Met	Gly	Lys	Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	
3675		2095	5				2100	)				210	5				
3676																	
3677					AGC												6384
3678	Thr	Met	Pro	Thr	Ser	Leu	Pro	Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	
3679	2110	)				2115	5				2120	)				2125	
3680																	
3681	AAG	GGT	AGT	AGG	AGG	AAG	AAG	TCT	CTG	AGT	GAG	AAG	GTC	CAA	CTG	TCT	6432
3682	Lys	Gly	Ser	Arg	Arg	Lys	Lys	Ser	Leu	Ser	Glu	Lys	Val	${\tt Gln}$	Leu	Ser	
3683					2130	)				2135	5				2140	)	
3684																	
3685					ACT												6480
3686	Glu	Ser	Ser	Val	Thr	Leu	Ser	Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	
3687				214	5				2150	)				2155	5		
3688																	
3689					GAC												6528
3690	Thr	Tyr	Val	Ser	Asp	Thr	Thr	Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	
3691			2160	)				2165	5				2170	)			
3692																	
3693					TCA												6576
3694	Ile			Ala	Ser	Pro			Met	Leu	Ala			Ala	Pro	Pro	
3695		2179	5				2180	)				218	5				
3696																	
3697					GCC												6624
3698			Val	His	Ala			Ala	Leu	Ser			Asn	Leu	His		
3699	2190	)				2199	5				2200	)				2205	
3700						~	~~~	~~~				~	~~~				
3701					GCA												6672
3702	Met	GIn	Pro	Leu	Ala		GLY	Ala	Ser			Leu	Pro	Ser			
3703					2210	)				2215	5				2220	ט	
3704	a. a	mma	am.	maa	a	a . a	a	3 mm	ama	mam	~~~	~~~	3 am	~~~	3 CM	a a m	6700
3705					CAC												6720
3706	GIII	ьeu	ьeu		His -	HIS	HIS	тте			Pro	GIA	ser	_		Ala	
3707 3708				2225	•				2230	,				2235	•		
3708	CCA	7\CC	mma	א כיתי	AGG	CTC	CAT	CCA	CTC	CCA	CTC	CCA	CCA	CAT	TOO	አጥሮ	6768
3710					Arg												0/00
3711	GIY	Ser	2240		Arg	пеп	птэ	2245		PIO	vai	PIO	2250	-	тъ	Mec	
3712			224(	,				224.	,				223	,			
3712	አአሮ	ccc	λтС	CAC	GTG	א א ידי	GVG	אככ	CVC	<b>ጥ</b> አ <i>ር</i>	ייי א א	GAG	አጥር	արդուր	сст	አጥር!	6816
3713					Val												0010
3714	voii	2255		GIU	val	woll	2260		GIII	- Y -	woll	226!		E 11G	OLY	1.100	
3716		223.	,				2200	,				220.	,				
3717	GTC	СТС	GCT	CCA	GCT	GAG	GGC	ACC	САТ	ССТ	GGC	ΔΤΔ	GCT	כככ	CAG	AGC	6864
3717					Ala												000±
3719	2270			0		2275	_				228					2285	
3720	/	-				/ .	-					-					
3721	AGG	CCA	CCT	GAA	GGG	AAG	CAC	ATA	ACC	ACC	CCT	CGG	GAG	CCC	TTG	CCC	6912
3722					Gly												
3723					2290	_				229					2300		

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3724									
3725	CCC ATT GTG ACT TTC CAG CTC ATC CCT AAA GGC AGT ATT GCC CAA CCA 69	<b>5</b> 0							
3726	Pro Ile Val Thr Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro	, 0							
3727	2305 2310 2315								
3728	2505 2510 2515								
3729	GCG GGG GCT CCC CAG CCT CAG TCC ACC TGC CCT CCA GCT GTT GCG GGC 70	าล							
3730	Ala Gly Ala Pro Gln Pro Gln Ser Thr Cys Pro Pro Ala Val Ala Gly	, 0							
3731	2320 2325 2330								
3732	2320 2323 2330								
3733	CCC CTG CCC ACC ATG TAC CAG ATT CCA GAA ATG GCC CGT TTG CCC AGT 70:	56							
3734	Pro Leu Pro Thr Met Tyr Gln Ile Pro Glu Met Ala Arg Leu Pro Ser	, ,							
3735	2335 2340 2345								
3736									
3737	GTG GCT TTC CCC ACT GCC ATG ATG CCC CAG CAG GAC GGG CAG GTA GCT 710	14							
3738	Val Ala Phe Pro Thr Ala Met Met Pro Gln Gln Asp Gly Gln Val Ala								
3739	2350 2355 2360 2365								
3740									
3741	CAG ACC ATT CTC CCA GCC TAT CAT CCT TTC CCA GCC TCT GTG GGC AAG 71	52							
3742	Gln Thr Ile Leu Pro Ala Tyr His Pro Phe Pro Ala Ser Val Gly Lys								
3743	2370 2375 2380								
3744									
3745	TAC CCC ACA CCC CCT TCA CAG CAC AGT TAT GCT TCC TCA AAT GCT GCT 72	00							
3746	Tyr Pro Thr Pro Pro Ser Gln His Ser Tyr Ala Ser Ser Asn Ala Ala								
3747	2385 2390 2395								
3748									
3749	GAG CGA ACA CCC AGT CAC AGT GGT CAC CTC CAG GGT GAG CAT CCC TAC 724	18							
3750	Glu Arg Thr Pro Ser His Ser Gly His Leu Gln Gly Glu His Pro Tyr								
3751	2400 2405 2410								
3752									
3753	CTG ACA CCA TCC CCA GAG TCT CCT GAC CAG TGG TCA AGT TCA TCA CCC 72:	96							
3754	Leu Thr Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser Ser Ser Pro								
3755	2415 2420 2425								
3756									
3757	CAC TCT GCT TCT GAC TGG TCA GAT GTG ACC ACC AGC CCT ACC CCT GGG 734	14							
3758	His Ser Ala Ser Asp Trp Ser Asp Val Thr Thr Ser Pro Thr Pro Gly								
3759	2430 2435 2440 2445								
3760									
3761	GGT GCT GGA GGA GGT CAG CGG GGA CCT GGG ACA CAC ATG TCT GAG CCA 73	€2							
3762	Gly Ala Gly Gly Gln Arg Gly Pro Gly Thr His Met Ser Glu Pro								
3763	2450 2455 2460								
3764									
3765	CCA CAC AAC AAC ATG CAG GTT TAT GCG TGAGAGAGTC CACCTCCAGT 74:	39							
3766	Pro His Asn Asn Met Gln Val Tyr Ala								
3767	2465 2470								
3768	CONTRACTOR AND AND CONTRACTOR OF CONTRACTOR	20							
3769	GTAGAGACAT AACTGACTTT TGTAAATGCT GCTGAGGAAC AAATGAAGGT CATCCGGGAG 74:	7 ブ							
3770 3771	AGAAATGAAG AAATCTCTGG AGCCAGCTTC TAGAGGTAGG AAAGAGAAGA TGTTCTTATT 75	<b>.</b> 0							
3772	73: TIALLITIEL MOMMONAMA DOLLAGOLIC IMONOGINOG MANGAMAMA IGIICITALI (73)	כנ							
3773	CAGATAATGC AAGAGAAGCA ATTCGTCAGT TTCACTGGGT ATCTGCAAGG CTTATTGATT 76	19							
3774	ondining to the state of the st								
J , , I									

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3775 3776	ATTCTAATCT	AATAAGACAA	GTTTGTGGAA	ATGCAAGATG	AATACAAGCC	TTGGGTCCAT	7679
3777 3778	GTTTACTCTC	TTCTATTTGG	AGAATAAGAT	GGATGCTTAT	TGAAGCCCAG	ACATTCTTGC	7739
3779 3780	AGCTTGGACT	GCATTTTAAG	CCCTGCAGGC	TTCTGCCATA	TCCATGAGAA	GATTCTACAC	7799
3781 3782	TAGCGTCCTG	TTGGGAATTA	TGCCCTGGAA	TTCTGCCTGA	ATTGACCTAC	GCATCTCCTC	7859
3783 3784	CTCCTTGGAC	ATTCTTTTGT	CTTCATTTGG	TGCTTTTGGT	TTTGCACCTC	TCCGTGATTG	7919
3785 3786	TAGCCCTACC	AGCATGTTAT	AGGGCAAGAC	CTTTGTGCTT	TTGATCATTC	TGGCCCATGA	7979
3787 3788	AAGCAACTTT	GGTCTCCTTT	CCCCTCCTGT	CTTCCCGGTA	TCCCTTGGAG	TCTCACAAGG	8039
3789 3790	TTTACTTTGG	TATGGTTCTC	AGCACAAACC	TTTCAAGTAT	GTTGTTTCTT	TGGAAAATGG	8099
3791 3792	ACATACTGTA	TTGTGTTCTC	CTGCATATAT	CATTCCTGGA	GAGAGAAGGG	GAGAAGAATA	8159
3793 3794	CTTTTCTTCA	ACAAATTTTG	GGGGCAGGAG	ATCCCTTCAA	GAGGCTGCAC	CTTAATTTTT	8219
3795 3796	CTTGTCTGTG	TGCAGGTCTT	CATATAAACT	TTACCAGGAA	GAAGGGTGTG	AGTTTGTTGT	8279
3797 3798	TTTTCTGTGT	ATGGGCCTGG	TCAGTGTAAA	GTTTTATCCT	TGATAGTCTA	GTTACTATGA	8339
3799 3800	CCCTCCCCAC	TTTTTTAAAA	CCAGAAAAAG	GTTTGGAATG	TTGGAATGAC	CAAGAGACAA	8399
3801 3802	GTTAACTCGT	GCAAGAGCCA	GTTACCCACC	CACAGGTCCC	CCTACTTCCT	GCCAAGCATT	8459
3803 3804	CCATTGACTG	CCTGTATGGA	ACACATTTGT	CCCAGATCTG	AGCATTCTAG	GCCTGTTTCA	8519
3805 3806	CTCACTCACC	CAGCATATGA	AACTAGTCTT	AACTGTTGAG	CCTTTCCTTT	CATATCCACA	8579
3807 3808	GAAGACACTG	TCTCAAATGT	TGTACCCTTG	CCATTTAGGA	CTGAACTTTC	CTTAGCCCAA	8639
3809 3810	GGGACCCAGT	GACAGTTGTC	TTCCGTTTGT	CAGATGATCA	GTCTCTACTG	ATTATCTTGC	8699
3811 3812	TGCTTAAAGG	CCTGCTCACC	AATCTTTCTT	TCACACCGTG	TGGTCCGTGT	TACTGGTATA	8759
3813 3814	CCCAGTATGT	TCTCACTGAA	GACATGGACT	TTATATGTTC	AAGTGCAGGA	ATTGGAAAGT	8819
3815 3816	TGGACTTGTT	TTCTATGATC	CAAAACAGCC	CTATAAGAAG	GTTGGAAAAG	GAGGAACTAT	8879
3817 3818	ATAGCAGCCT	TTGCTATTTT	CTGCTACCAT	TTCTTTTCCT	CTGAAGCGGC	CATGACATTC	8939
3819 3820	CCTTTGGCAA	CTAACGTAGA	AACTCAACAG	AACATTTTCC	TTTCCTAGAG	TCACCTTTTA	8999
3821 3822	GATGATAATG	GACAACTATA	GACTTGCTCA	TTGTTCAGAC	TGATTGCCCC	TCACCTGAAT	9059
3823 3824	CCACTCTCTG	TATTCATGCT	CTTGGCAATT	TCTTTGACTT	TCTTTTAAGG	GCAGAAGCAT	9119
3825	TTTAGTTAAT	TGTAGATAAA	GAATAGTTTT	CTTCCTCTTC	TCCTTGGGCC	AGTTAATAAT	9179

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3826							
3827	TGGTCCATGG	CTACACTGCA	ACTTCCGTCC	AGTGCTGTGA	TGCCCATGAC	ACCTGCAAAA	9239
3828							
3829	TAAGTTCTGC	CTGGGCATTT	TGTAGATATT	AACAGGTGAA	TTCCCGACTC	TTTTGGTTTG	9299
3830							
3831	AATGACAGTT	CTCATTCCTT	CTATGGCTGC	AAGTATGCAT	CAGTGCTTCC	CACTTACCTG	9359
3832							
3833	ATTTGTCTGT	CGGTGGCCCC	ATATGGAAAC	CCTGCGTGTC	TGTTGGCATA	ATAGTTTACA	9419
3834							
3835	AATGGTTTTT	TCAGTCCTAT	CCAAATTTAT	TGAACCAACA	AAAATAATTA	CTTCTGCCCT	9479
3836	~~~~~	~	~~~~~				
3837	GAGATAAGCA	GATTAAGTTT	GTTCATTCTC	TGCTTTATTC	TCTCCATGTG	GCAACATTCT	9539
3838	CMC2 CCCMCM	mmaa ma amam	CC3 3 3 C3 MMM	<b>#</b> 3 #G3 ##G#3	3 3 maamaa am	~~~~~~~~~	0500
3839 3840	GTCAGCCTCT	TTCATAGTGT	GCAAACATTT	TATCATTCTA	AATGGTGACT	CTCTGCCCTT	9599
3841	GGACCCATTT	አ ጥጥ አ ጥጥ ረ አ ረ አ	CATCCCCACA	ACCTATCTGC	איזיים אינים מעריים ביים אינים אינים אינים אינים אינים אינים מעריים אינים אינים אינים אינים אינים אינים אינים אינים אינים אינ	A COA TOOTTO	9659
3842	GGACCCATTT	ATTATTCACA	GAIGGGGAGA	ACCIAICIGC	AIGGACCCIC	ACCATCCTCT	9009
3843	GTGCAGCACA	CACAGTGCAG	CCACCCACTC	GCGATGGCGA	TGACTTTCTT	CCCCTGGGAA	9719
3844	GIGCHGCHCH	CHCHGIOCHG	GONGCCAGIO	OCOATOCCA	IGACITICIT	CCCCIGGAA	J11J
3845	TTCC						9723
3846							3,23
3847							

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APPLICATION NUMBER FILING DATE PRIOR APPLICATION DATA

## SEQUENCE CORRECTION REPORT PATENT APPLICATION US/08/083,590

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Corrected Text